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Result
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Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d. No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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length: 2000000000
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/BTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfIles1.seq:*
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Listing first 45 summaries
     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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     BB
US-07-745-206A-12
US-08-311-363-12
US-08-311-363-12
US-08-232-463-14
US-08-456-200B-11
US-09-072-596-179
US-09-072-596-179
US-09-072-596-179
US-08-455-543A-8
US-08-49-386-8
US-08-49-386-8
US-08-49-386-8
US-08-49-386-8
US-08-48-709A-8
US-08-48-709A-8
US-08-48-709A-7
US-08-193-078B-7
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Sequence 12, Appl
Sequence 14, Appl
Sequence 17, Appl
Sequence 8, Appli
Sequence 7, Appli
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                     US-07-745-206A-12
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28 49 3.8 736.4 US-09-268-163-5 30 49 3.8 7376.4 US-09-268-163-3 31 48 3.8 4403765 3 US-09-268-163-3 32 46.6 3.6 745 1 US-08-469-569-163 33 46.6 3.6 745 1 US-08-469-522A-163 36 46.6 3.6 745 1 US-08-469-522A-163 37 46.6 3.6 745 1 US-08-469-526A-163 38 46.6 3.6 745 2 US-08-469-526A-163 39 46.6 3.6 745 2 US-08-469-60-163 39 46.6 3.6 745 3 US-08-470-335-163 39 46.6 3.6 745 3 US-08-470-335-163 30 46.6 3.6 745 3 US-08-734-018-51 30 46.6 3.6 745 3 US-08-734-018-51 31 46.6 3.6 745 3 US-08-735-021-163 32 46.6 3.6 745 3 US-08-735-021-163 33 46.6 3.6 745 3 US-08-735-021-163 34 46.6 3.6 745 3 US-08-735-021-163 35 46.6 3.6 745 3 US-08-735-021-163 36 46.6 3.6 745 3 US-08-735-021-163 37 46.6 3.6 745 3 US-08-735-021-163 38 46.6 3.6 745 3 US-08-735-021-163 39 46.6 3.6 745 3 US-08-735-021-163 30 46.6 3.6 745 3 US-08-735-021-163 30 46.6 3.6 745 5 PCT-US94-05083C-159
49 3.8 7364 4 US-09-268-163-3 49 3.8 7376 4 US-09-268-163-3 49 3.8 7376 1 US-09-268-163-3 48 3.8 4403765 3 US-09-103-840A-1 46.6 3.6 745 1 US-08-249-322A-1 46.6 3.6 745 2 US-08-469-560-163-1 46.6 3.6 745 2 US-08-341-018-51 46.6 3.6 745 3 US-08-341-018-51 46.6 3.6 745 3 US-08-31-035-163-1 46.6 3.6 745 3 US-08-31-035-163-1 46.6 3.6 745 3 US-08-31-035-163-1 46.6 3.6 745 3 US-08-31-039-163-1 46.6 3.6 745 5 PCT-US95-08846A-1
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4 US-09-268-163-3 4 US-09-268-163-3 5 US-09-103-840A-1 1 US-08-469-569-16 1 US-08-469-569-16 1 US-08-469-526A-16 1 US-08-469-569-16 1 US-08-479-328A-1 1 US-08-479-328A-1 1 US-08-479-328-1 1 US-08-479-328-1 1 US-08-470-335-1 2 US-08-470-335-1 3 US-08-734-684-1 3 US-08-734-684-1 3 US-08-734-684-1 5 PCT-US94-0503-16
US-09-268-163-3 US-09-268-163-3 US-09-268-163-3 US-09-103-840A US-08-036-555B-16 US-08-0469-569-16 US-08-469-526A-16 US-08-469-526A-16 US-08-4734-591A-11 US-08-471-018-51 US-08-471-018-51 US-08-471-018-51 US-08-734-664A-16 US-08-734-664A-16 US-08-470-339-166 US-08-470-339-166 US-08-470-339-166 US-08-470-339-166 US-08-470-339-166
US-08-450-273-7 US-09-268-163-3 US-09-268-163-3 US-09-268-163-3 US-08-05-5558-163 US-08-469-569-163 US-08-469-528-163 US-08-469-528-163 US-08-469-526-163 US-08-470-335-163 US-08-735-021-163

ALIGNMENTS

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RESULT 1

US-07-745-206A-12

Sequence 12, Application US/07745206A
Patent No. 5429921

GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Harpold, Michael
APPLICANT: Holdman, Daniel
TITLE OF INVENTION:
APPLICANT: Feldman, Daniel
TITLE OF INVENTION:
Methods

INTERSONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSE: Fitch, Even, Tabin & Flannery
STREET: 135 S. LaSalle
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.

ZIP: 60603
ZIP: 60603
ZIP: 60603
ZIP: FOODS/MS-DOS
SOPTARE: Patentin Release #1.0, Version #1.25
CORPUTER: BADBLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: LIMP C Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURLETT APPLICATION INFORMATION:
ARPLICATION INFORMATION:
NAME: Feder: SCOCT B
REFERENCE/DOCKET NUMBER: 51504
TELEPHONE: 312-372-7842
INFORMATION EVEN SOCIES
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RESULT 2
US-08-311-363-12
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Best Local S
Matches 171
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                        NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-51506
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/311,363
                                                                                                                                                                                       ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin,
                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Brenner, Robert
TITLE OF INVENTION: Human Calcium Channel Compositions
TITLE OF INVENTION: Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
             TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity nes 171; Conserv
                                                                                                                                       FILING DATE
                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                           CITY: San Diego
STATE: California
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5876958
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                                                                                                                                                                                                                                                                                                                                                                                                    McCue, Ann
(619)238-0062
                                                                                                                                                                                                                                                                                                                                                                                                               Williams, Mark
Feldman, Daniel
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Ellis, Steven
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                (619)238-0999
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                                                                                                                                       DATA:
.R: US/08/311,363
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Pred. No. 0.00037;
0; Mismatches 195; Indels
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                                                                                                                                                                                                                                                                                                         Sequence 14, Application US/08232463 Patent No. 5670367
                                                                                                                                                                                                                                                                                                       Patent No.
                      ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release 4.
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                                                                                                                                                                                                            APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT
NUMBER OF SEQUENCES: 52
CURRENT APPLICATION D
APPLICATION NUMBER:
                                                                                                                                                                                                                                            APPLICANT: DORNER, F. APPLICANT: SCHEIFLINGER, APPLICANT: FALKNER, F. G.
                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 5467 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: FEATURE:
                                                                                                                                       CITY: Alexandria STATE: VA
                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
LOCATION:
LOCATION:
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LOCATION:
LOCATION:
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Local Similarity 46.7%;
es 171; Conservative
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                                                                                                                                                                   E: Foley & Lardner
                           PatentIn Release #1.0,
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..3392, 3396..3488, 3495..3559, 3543..3581, 3585
..3587, 3591..3626, 3630..3689, 3693..3737, 3744
...3746, 3750..4823, 4827..4841, 4845..5006, 5010
...5096, 5100..5306, 5310..5366, 5370..5465)
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E: DNA (genomic)
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              DATA:
US/08/232,463
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Pred. No. 0.00037;
                                                                                                                                                                   Suite 500
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                                                                                                                                                                                                                                 FOWLPOX VIRUS
                             Version
                               #1.25
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COUNTRY: U.S.A

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RESULT 4
US-08-456-200B-11
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US-08-232-463-14
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Best Local S
Matches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/08456200B Patent No. 6229000
                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Franz, Jurgen; Weingartner, Bernhard;
APPLICANT: Unterbeck, Axel; Rae, Peter
TITLE OF INVENTION: TISSUE-SPECIFIC HUMAN NEURONAL
TITLE OF INVENTION: CALCIUM CHANNEL SUB-TYPES AND
TITLE OF INVENTION: THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 899149
INFORMATION FOR SEQ ID NO:
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REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: EP 91
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STREET: 500
CITY: Tarrytown
CTATE: New York
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APPLICATION NUMBER:
                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
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4.2%; Score 53.2; DB 1;
Local Similarity 6.5%; Pred. No. 0.00068;
hes 25; Conservative 202; Mismatches 155;
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                                                                                                          E: SPRUNG HORN KRAMER & WOODS
660 White Plains Road
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Best Local Similarity 48.0%;
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FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/094,712
FILING DATE: 19-7UL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/858,278
FILING DATE: 26-MAR-1992
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PRIOR APPLICATION NUMBER: 08/06
APPLICATION NUMBER: 08/06
APPLICATION TIPMY-1993
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
MEDIUM TYPE: Storage
MEDIUM TYPE: STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: Nucleotide
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: cDNA
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APPLICATION NUMBER: DE 41
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: Bayer 8398.3-KGB
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REGISTRATION NUMBER:
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CACGAGGCTGTGGAGAAGGAGACCACNGAGAAGGAGGCCACGGAGAAGGAGGCTGAGAT 2051
                                                                                                                                                                                                               GAGCGGGAGCCCCGACCCCACCGCGCACCGGCACCAGGATCCGAGCAAGGAGTGCGCC 1872
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                                                                      GCGGAGAGCGGGGAGGAGCCGGCGCGGCGCACCGGGCCCCGGCACAAGGCGCAGCCTGCT 1992
                                                                                                      GCCCCAAGGGCGAGCGGNGNGCGCGGCACCGCGGCGGCCCCGAGCGGGGCCCCGGGAG
                                                                                                                                                                           GGGCAGGCCGGGTGGGAGCAGCAGCCACCGCAGGACCGGAACAGTGTGGCGGCGAT 668
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Pred. No. 0.0027;
0; Mismatches 215; Indels
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                                                                                                                                 US-09-072-596-174
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                           Sequence 174, Applicate Patent No. 6458366 GENERAL INFORMATION:
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Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/99/056,556
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Best Local :
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TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO:
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APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 400 base pairs
TYPE: nucleic acid
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REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 211
TELECOMMUNICATION INFORMATION:
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APPLICANT:
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TOPOLOGY: li
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o. 6350456
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                                                                                           Application US/09072596
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Steven G.
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Pred. No. 0.0015;
0; Mismatches 134;
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US-09-072-967-179

Sequence 179, Application US/09072967 Patent No. 6592877 GENERAL INFORMATION: APPLICANT: Reed, Steven G. APPLICANT: Skeiky, Yasir A.W.

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INFORMATION FOR SEQ ID NO: 17
SEQUENCE CHARACTERISTICS:
LENGTH: 400 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: 1BM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION UNMBER: US/09/072,596

FILING DATE: 05-MAY-1998

CLASSIFICATION:

CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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APPLICANT:
APPLICANT:
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APPLICANT:
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                           GTCCTGCCGCAGAGATGGCTCAGG
CGGCGGCGACGGTGCACTCTCAGG
                                                                               Washington
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6300 Columbia Center, 701 Fifth Avenue
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Hendrickson, Ronald C.
JENTION: COMPOUNDS AND
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Vedvick, Thomas S.
Twardzik, Daniel R.
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Dillon, Davin C.
Campos-Neto, Antonia
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Pred. No. 0.0015;
0; Mismatches 134;
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RESULT 8
US-08-455-543A-8
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US-09-072-967-179
                                               Sequence 8, Application US/08455543A Patent No. 5792846
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GENERAL INFORMATION:
APPLICANT: Harpol
APPLICANT: Ellis,
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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APPLICANT:
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LENGTH: 400 base pairs
TYPE: nucleic acid
STRANDEDNESS; single
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APPLICATION NUMBER: US/09/072,967
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 355
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Vedvick, Thomas S.
Twardzik, Daniel R.
Twardzik, Michael J.
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6300 Columbia Center,
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 Harpold, Michael
Ellis, Steven
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Pred. No. 0.0015;
0; Mismatches 134; Indels
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; NAME/KEY:
; LOCATION:
US-08-455-543A-8
Query Match
Best Local Similarity
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APPLICATION DATA:
APPLICATION NUMBER: US 07/600
PRIOR ADDITE: 04-500
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/223,305

FILING DATE: April 4, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/868,354

FILING DATE: April 10, 1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/745,20
                                                                                                                                                                                                                                                                              TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7175 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION UNMBER: WO ECT/
FILING DATE: 04-APP-1000
PRIOR ADDITE: 04-APP-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION UNBER: WO PCT/US89/01408
PRIOR APPLICATION UNBER: US 07/177
FILING DATE: 04-APP
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APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN C.
TITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,543A
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ADDRESSEE: Brown, Martin,
                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (619)238-0999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                              NAME: Seidman, Stephanie L. REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 63
                                                                                                                                                                NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                             TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
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                                                                                                                   LOCATION:
                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                               STRANDEDNESS:
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Feldman, Daniel
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SYSTEM: DOS
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6855..7175
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   3.8%;
48.0%;
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   Score 49;
Pred. No.
   DB 1;
0.0085;
                 Length 7175;
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RESULT 9
US-08-193-078B-8
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                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 10-APR-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                APPLICATION NUMBER: US 07/745,206 FILING DATE: 15-AUG-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                 SOFTWARE: Patentin Rel
                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
               ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   PPLICANT:
                                       NAME: Seidman, Stephanie L. REGISTRATION NUMBER: 33,779
                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 07-FEB CLASSIFICATION: 435
                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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1660 UNION STREET
                                                                                                                                                                                                                                                                                               USA
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VENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
ZENTION: METHODS
EQUENCES: 29
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Ellis, Steven
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Feldman, Daniel
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                                                                                                                                                                       07~FEB-1994
                                                                                                                                   US 07/868,354
                                                                                                                                                                                                               Release #1.0, Version #1.25
                                                                                                                                                                                    US/08/193,078B
                                      33,779
                            6362-53607
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                                                                                                                                                                                                                                       Sequence
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Best Local Similarity
Matches 201; Conserv
                                                                                                                                                                                                                         Patent No.
                                                                                                    APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: METHODS
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NAME/KEY:
                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin,
                                                                                          NUMBER OF SEQUENCES:
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                         CITY: San Diego
STATE: California
                                                     STREET:
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LOCATION:
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LOCATION:
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92101-2926
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CALCIUM CHANNEL COMPOSITIONS AND

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SEQUENCE CHARACTERISTICS:
LENGTH: 7175 base pair
250 GACGCTGCGGTGCAGGTGAACCCGCGCGCGCGACGCCTCGGTGCAGTGTTCACTCGGGCCGC
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                                                                                        GTGGCCGCGAGGAAAGCGGTCCCCCAGCCGCGAAGCGAGGAGGGCGATGTTCAGGCTGCA 609
                                                                                                                        GGCGCCAAGGGGGCGCGCGCGCGCGCACCGGGGCCCCCGAGCGGGGCCCCCGGGAG
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6855..7175
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0.0085;
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US-08-223-305C-8
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Best Local
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APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                           3.8%;
Local Similarity 48.0%;
les 201; Conservation
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ Version 1.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPLICATION NUMBER:
2928
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GAGCGGGAGCCCCGACCCCACCGCGCACCGGCACCAGGATCCGAGCAAGGAGTGCGCC 2987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
                                                          CCCCGTGGCCACGCCGGCGCGCGAGATCCCCGCGATCCTGGCAGACCGTAGCCCCGTTC
                            CATION DATA:
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6855..7175
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20-FEB-1990
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30-NOV-1990
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US-08-149-097D-8
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER: US/0
FILING DATE: 05-NOV-1993
                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 15-AUG-1991
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PRIOR APPLICATION DATA:
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                                                                                                                                              APPLICATION NUMBER: US 0 FILING DATE: 20-FEB-1990
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                                  APPLICATION NUMBER: WO PILING DATE: 04-APR-1989
                                                                                                            APPLICATION NUMBER:
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1660 Union Street
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Feldman, Daniel
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                                                                                        UMBER: US 07/603,751
04-APR-1989
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                                                    WO PCT/US89/01408
US 07/176,899
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Best Local Similarity
Matches 201; Conserv
                                                                                                                    GENERAL INFORMATION:
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TELEFAX: (619) 238-0062
INFORMATION FOR SEQ ID NO:
                                                                                         APPLICANT:
APPLICANT:
          APPLICANT: MCCue, Ann
APPLICANT: Gillespie, Alison
TITLE OF INVENTION: HUMAN CAI
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 38
                                                                          APPLICANT:
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CORRESPONDENCE ADDRESS:
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LOCATION:
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LOCATION:
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TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
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Ellis, Steven
Williams, Mark
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                                   CALCIUM CHANNEL COMPOSITIONS AND
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Best Local Similarity
Matches 201; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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NAME/KEY:
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NAME/KEY:
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 51
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: 08/
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APPLICATION NUMBER: 11-AUG-
APPLICATION NUMBER:
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LOCATION:
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STREET: 1660 Union Street
CITY: San Diego.
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GTGGCCGCGAGGAAAGCGGTCCCCCAGCCGCGAAGCGAGGAGGGCGATGTTCAGGCTGCA 609
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11-AUG-1993
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Pred. No.
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                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/914,231
FILING DATE: 13-JULY-1992
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APPLICATION NUMBER: 08/404,950
FILING DATE: 13-MAR-1995
APPLICATION NUMBER: 08/336,257
FILING DATE: 7-NOV-1994
                                                                                                                                             FILING DATE: 5-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/105,536
                                                                                                                                                                                                                                                PRIOR APPLICATION DAT APPLICATION NUMBER:
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FILING DATE: 23-SEPT-1994
PRIOR APPLICATION DATA:
08/290,012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: APPLICATION UNMBER: US/08/450,56; FILING DATE: CLASSIFICATION: 435
                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                             PRIOR APPLICATION DATA: 08/149,097
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                                 APPLICATION NUMBER: FILING DATE: 10-AP
                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 7-NOV-1994
UTOR APPLICATION DATA:
APPLICATION NUMBER: 08/314,083
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/223,305
                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 11-AU
                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 28-SEPT-1994
IOR APPLICATION DATA:
APPLICATION NUMBER: 08/31
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1660 Union Street
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VENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS
VENTION: METHODS
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Gillespie, Alison
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Ellis, Steven
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                                 MBER: 07/868,354
10-APR-1992
                                                                                                                                                                                                                                      DATA:
RER: 08/193,078
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PCT/US92/06903
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US-08-450-562-8
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 7175 base pairs
TYPE: nucleic acid
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Best Local Similarity
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LOCATION:
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LOCATION:
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REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                              2988 GGCGCCAAGGGCGAGCGCGCGCGCGCACCGGCGGCCCCCGAGCGGGGCCCCGGGAAG
                                                                                                                                                              2928 GAGCGGGAGCCCCGACGCCACCGCGCGCACCGGCACCAGGATCCGAGCAAGGAGTGCGCC 2987
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                                                                                                                                                                                                                                                                                                                             310 CGCACGCTGCAGCCTGCAGGGTGCCGAGCCAGCCCGACGCCCGATCGGGTTCCTGTCAA 369
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GGGCAGGCCGGGTGGGAGCAGCCACCACCGGAGGACCGGAACAGTGTGGCGGCGAT 668
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08-NOV-1990
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US-08-984-709A-8
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Best Local Similarity
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY:
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REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24735-9815 (formerly 6362-9815)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 450-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE
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MEDIUM TYPE: Diskett
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T: 4250 Executive Square, Suite 700
La Jolla
: California
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 CCCCGTGGCCACGCCGGGGAGATCCCCGCGATCCTGGCAGACCGTAGCCCCGTTC
                                                                                           CGCACGCTGCAGCCTGCAGGGTGCCAAGCCAGCCCGACGCCCGATCGGGTTCCTGTCAA
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6855..7175
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0; Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                               FILING DATE: 28-SEPT-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,277
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APPLICANT:
APPLICANT:
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                         PRIOR APPLICATION DATA:
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CLASSIFICATION DATA:
                                       APPLICATION NUMBER: 08/1
FILING DATE: 07-FEB-1994
                                                                                                      APPLICATION NUMBER: 08/
FILING DATE: 4-APR-1994
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                                                                                           CLASSIFICATION:
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Gillespie, Alison
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Ellis, Steven
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                                                                                                                                                                  11-AUG-1994
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ROBert
HUMAN CALCIUM CHANNEL COMPOSITIONS AND
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08/149,097
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FEATURE:
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Best Local Similarity 48.0%;
Matches 201; Conservative
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 7175 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06903
FILING DATE: 14-AUG-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/745,206
FILING DATE: 15-AUG-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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NAME/KEY:
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REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-519812
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 238-0999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
PILING DATE: 10-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA: 07/914,231
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3048 GCGGAGAGCGGGAGGAGCCGGCGCGGCGCACCGGGCCCGGCACAAGGCCGCAGCCTGCT 3107
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                                   550 GTGGCCGCGAGGAAAGCGGTCCCCCAGCCGCGAAGCGAGGAGGGCGATGTTCAGGCTGCA 609
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                                                                                                           250 GACGCTGCGGTGCAGGTGAACCCGCGCGCGACGCCTCGGTGCAGTGTTCACTCGGGCGC 309
                                                                       GECECAAGGGCGAGCGGCGCGCGCGCACCGCGGCGCCCCCGAGCGGGCCCCCGGGAG
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3: DNA (genomic)
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11-AUG-1993
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Qy 610 GGGCAGGCCGGGTGGGAGCAGCCACCGGAGGAACAGTGTGGCGGCGAT 668

Search completed: April 6, 2004, 20:38:15 Job time : 138 secs

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 2000000000
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   643.4
642.4
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Gapop 10.0 , Gapext 1.0
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   50.4
46.3
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Copyright (c) 1993 - 2004 Compugen Ltd.
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gb_est2:*
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ALIGNMENTS

RESULT 1

TITLE JOUENAL COMMENT	AUTHORS	SOURCE ORGANISM	ACCESSION VERSION KEYWORDS	BB641267 LOCUS DEFINITION
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramateu, M. and Hayashizaki, Y. RIKEN Mouse ESTs (Arakawa, T., et al. 2001) Unpublished (2001) Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan	Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Arrakawa,T., Carninci,P., Fukuda,S., Furuno,M., Kawai,J., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Salto,R., Sakai,C., Sakai,K.,	Mus musculus (house mouse) Mus musculus Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	musculus cDNA clone A830014H23 5', mRNA sequence. B8641267 B8641267.1 GI:16476392 EST:	BB641267 RIKEN full-length enriched. 10 days neonate cortex Mus

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Query Match
Best Local Similarity
                              406
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Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yananaka,I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Watahiki, M., Sheda, T., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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URL:http://genome.gsc.riken.go.jp/
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     TCCTGGCAGACCGTAGCCCCGTTCTCGTCCGTGACCTTCTGTGGCCTCTCCTCCTCACTG
                                                                                                          GACGCCCGATCGGGTTCCTGTCAACCCCGTGGCCACGCCGGCGCCGGGAGATCCCCCGGGA
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81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="cortex"
/dev_stage="10 days neonate"
/lab_host="DH10B"
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/db_xref="taxon:10090"
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E 1 (bases 1 to 666)

Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sagube,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y. Takada,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y. RIKEN Mouse ESTs (Arakawa,T., et al. 2001)

On Jul 7, 2000 this sequence version replaced gi:8960678.
Contact: Yoshinide Hayashizaki
Contact: Yoshinide Hayashizaki
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
Tal. 45.50.2022
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BB264222
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.p., Shibata,Y., Hayatsu,N.,
Itoh,M., Konno,H., Okazaki,Y., Murama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              musculus cDNA clone A83
BB264222
BB264222.2 GI:16400187
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                                                                                                   Fax: 81-45-503-9216
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RIKEN full-length enriched, 10 days neonate cortex Mus
cDNA clone A830014H23 3', mRNA sequence.
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     su,N., Sugahara,Y., Shibata,K.,
Muramatsu,M. and Hayashizaki,Y
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659 945 600 885 540 825 480 765 420 705 360 645 300 585 240

FEATURES

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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA Computer-based methods for the mouse full-length cDNA construction of an encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Kaizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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Please visit our web site (http://genome.gsc.riken.go.jp/)
further details.
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                                                                                                                                                                                                                                                                                                 50.3%; llarity 99.6%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Rome Genome Exploration ferome Caboratory in Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clo\overline{n}e lib="RIKEN full-length enriched, 10 days neonate cortex"
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/dev_stage="10 days neonate"
/lab_host="DH108"
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/db_xref="taxon:10090"
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                                                               National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details. Plate: H3102 row: B column: 03
Seq. primer: -21M13 Forward
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H3102B03 3', mRNA sequence.
BG071693
BG071693.2 GI:40072037
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Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X.,
Tanaka,T.S., Jaradat,S.A., Sano,Y., Piao,Y., Nagaraja,R., Doi,E
Grahovac,M.J., Pantano,S., Sano,Y., Piao,Y., Nagaraja,R., Doi,E
Wood,W.H. III, Becker,K.G. and Ko,M.S.H.
Genome-wide expression profiling of mid-gestation placenta and
embryo using a 15,000 mouse developmental cDNA microarray
embryo using a 15,000 mouse developmental cDNA microarray
Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
                                                                                                                                                                                                                                                                                              On Jan 26, 2001 this sequence version replaced gi:12554262 Other_ESTs: H3102B03-5
                                                                                                                                                                                                                         Laboratory of Genetics National Institute on !
                                                                                                                                                                                                                                                              Contact: George J. Kargul
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                             quality sequence stop: 615
Location/Qualifiers
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                                                                                             GAAAACGTTTCTGCTAGATGGGGCTAATGGAATGGACCAAGTGAGCTTTCTCCCCCTCTTCA 1182
                                                                                                                                                                                           GGACAAACGCCTGTCCTGCGACAGCATCCAGCTTCAAATACATCATTTAGTGAGAGTC 1122
                                                                                                                                                                                                                                          CAGACTTCGCCACGTGGACCCTAAACGCCCCCATCGGCAAGACTTGTGTGGGGAGATGCAA
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//clone lib="NIA Mouse 15K cDNA Clone Set"
//note="Vector: pspORT1; Site 1: SalI; Site 2: NotI; This
clone is among a rearrayed set of 15,247 clones from 11
embryo cDNA libraries (including preimplantation stage
embryos from unfertilized egg to blastocyst, embryonic
part of E77.5 embryos, extraembryonic part of E7.5
embryos, and E12.5 female mesonephros/gonad) and one
newborn ovary cDNA library. Average insert size 1.5 kb.
All source libraries are cloned unidirectionally with
Oligo(dT)-Not primers. References include: (1)
Genome-wide expression profiling of mid-gestation
placenta and embryo using a 15,000 mouse developmental
cDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97:
9127-9132; (2) Large-scale cDNA analysis reveals phased
gene expression patterns during preimplantation mouse
development, 2000, Development, 127: 1737-1749; (3)
Genome-wide mapping of unselected transcripts from
extraembryonic tissue of 7.5-day mouse embryos reveals
enrichment in the t-complex and under-representation on
the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."
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/strain="C57BL/6J"
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/mol_type="mRNA"
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Tanaka, T.S., Jaradat, S.A., Lim, M.K., Kargul, G.J., Wang, X., Grahovac, M.J., Pantano, S., Sano, Y., Piao, Y., Nagaraja, R., Doi, H., Wood, W.H. III, Becker, K.G. and Ko, M.S.H. Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community.
visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details
Plate: H3102 row: B column: 03
Seq.primer: -21M13 Reverse
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H3102B03-5 NIA Mouse 15K cDNA
H3102B03 5', mRNA sequence
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333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
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            /lab_host="DH10B"
/(clone lib="NIA Mouse 15K cDNA Clone Set"
/(clone lib="NIA Mouse 15K cDNA Clone Set"
//clone lib="NIA Mouse 15K cDNA Clone Set"
//clone lib="NIA Mouse 15K cDNA Clone Set of 15,247 clones from 11
embryo cDNA libraries (including preimplantation stage
embryos from unfertilized egg to blastcoyst, embryonic
part of B7.5 embryos, extraembryonic part of E7.5
embryos, and E12.5 female mesonephros/gonad) and one
newborn ovary cDNA library. Average insert size 1.5 kb.
All source libraries are cloned unidirectionally with
Oligo(dT) Not primers. References include: (1)
Genome-wide expression profiling of mid-gestation
placenta and embryo using a 15,000 mouse developmental
cDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97:
9127-9132; (2) Large-scale cDNA analysis reveals phased
gene expression patterns during preimplantation mouse
development, 2000, Development, 127: 1737-1749; (3)
Genome-wide mapping of unselected transcripts from
extraembryonic tissue of 7.5-day mouse embryos reveals
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/mol type="mRNA"
/strain="C57BL/6J"
/strain="C57BL/6J"
/db_xref="niaEST:H3102B03-5"
/db_xref="taxon:10090"
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UI-M-BH3-awu-b-08-0-UI 5', mRNA sequence.
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                        Contact: Chin, H
Mational Institute of Mental Health
MACOUNTY EXECUTIVE Blvd. Room 7N-7190, MSC 9643, Bethesda,
                                                                                               Genome Res. 6 (9),
97044477
                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 594) Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two approaches to facilitate gene
6001 Executive Blvd.
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
                                                                                                                           discovery
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h 44.7%; Similarity 99.5%; 93; Conservative CGCGAGGAAAGCGGTCCCCCAGCCGCGAAGCGAGGAGGGCGATGTTCAGGCTGCAGGGCA GGAGAGCGCCTATGTGTGTGTGTGCAGGGCACCAGTAAGGTG-TACTTCAAACAGTTCT GGAGAGCGCCTATGTGTGTGTGTGCAGGGCACCAGTAAGGTGTTACTTCAAACAGTTCT GGATGCCCCTCGAGACCAGGCCTCCCCGCAAAGCACGGAGCAGGACAAGGAGCGCCTGCG GGCCGGGTGGGAGCAGCAGCCACCGGAGGACCGGAACAGTGTGGCGGCGATGCAGTC GGCCGGGTGGGAGCAGCAGCCACCGCACGGAGGACCGGAACAGTGTGGCGGCGATGCAGTC TTTCCAGTTCTTAGAGCAGAAGTACGGCTACTATCACTGCAAGGACTGCAAAATCCGGTG TTTCCAGTTCTTAGAGCAGAAGTACGGCTACCTATCACTGCAAGGACTGCAAAATCCGGTG GGATGCCCCTCGAGACCAGGCCTCCCCGCAAAGCACGGAGCAGGACAAGGAGCGCCTGCG TGAGCCTGGGAGCGAGCCATGTCCTGCCGCAGAGATGGCTCAGGACCCCGGTGATTC CGCGAGGAAAGCGGTCCCCCAGCCGCGAAGCGAGGAGGGCGATGTTCAGGCTGCAGGGCA TGAGCCTGGGAGCGAGGAGCCATGTCCTGCCGCAGAGATGGCTCAGGACCCCCGGTGATTC Score 570.4; DB 10; Pred. No. 4.1e-76; 0; Mismatches 1; Indels Length 2 Gaps 535 475 674 614 914 295 854 355 794 415 734 2

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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                             Email: genome_res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
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and Hayashizaki,Y.
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e mouse tissues.
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
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Laboratory for Genome Exploration Research Group, RIKEN
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TTCGGATGCCCCTCGAGACCAGGCCTCCCCGCAAAGCACGGAGCAGGACAAGGAGCGCCT
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GACAGTGTTACTTGGATATAAAGCCTGTGAATAAAAAGGTATTGCAA 1257
                                                                                                                                                                                                                                     GTTGTAAAAGAACTAGATGTGCCCTGCCCAGTCAGATTTCGCCCACGTGGACCCTAAACGCC
                                                                                                                                                                                                                                                                                                                                                                                                  GCGTTTCCAGTTCTTAGAGCAGAAATACGGCTACTATCACTGCAAGGACTGCAAAAATCCG
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                                                                                                                             TCAGCTTCAAATACATCATTTAGTGAGAGTCGAAAAACGTTTCTGCTAGATGGGGCCTAATG 1151
                                                                                                                                                                                   CCCATCGGCAAGACTTGTGGGGAGATGCAAGGACAAACGCCTGTCCTGCGACAGCACCT
                                                                                                                                                                                                                     GTTGTAAAAGAACTAGATGTGCCTGCCCAGTCAGACTTCGCCACGTGGACCCTAAACGCC
                                                                                                                                                                                                                                                                              TCTGCCGAGTGTGTGAGAAATCCTACAACCCTTACAGAGTGGAGGACATCACCTGTCAAA
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                                       GAATGGACAAGTGAGCTTTCTCCCCTTCTTCACCTTTCCCTTTCCAAATTCTTCATGACA
                                                                                                 TCAGCTTCAAATACATCATTTAGTGAGAGTCGAAAACGTTTCTGCTAGATGGGGCTAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="in vitro fertilized eggs"
/dev_stage="egg"
/lab_host="PHHOB"
/clone_lib="RIKEN full-length enriched,
fertilized_eggs"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 497.2;
Pred. No. 4.1
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497; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mEST@mail.nih.gov
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized basal ganglia library cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined. Seq primer: M13 Forward POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Chin, H
National Institute of Mental Health
National Institute of Mental Health
National Institute Blvd. Room 7N-7190, MSC 9643, Bethesda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AI854700.1
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UI-M-BHO-akc-d-12-0-UI.s1 NIH BMAP M S1 Mus musculus cDNA clone
UI-M-BHO-akc-d-12-0-UI 3', mRNA sequence.
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                          TGCAAGGACTGCAAAATCCGGTGGGAGAGCGCCTATGTGTGGTGTGTGCAGGGCACCAGT 891
                                                                                                                    GAGCAGGACAAGGAGCGCCTGCGTTTCCAGTTCTTAGAGCAGAAGTACGGCTACTATCAC 831
                                                                                          GAGCAGGACAAGGAGCGCCTGCGTTTCCAGTTCTTAGAGCAGAAGTACGGCTACTATCAC
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                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                       /strain="C573L/60"
/db xref="taxon:10090"
/clone="UI-M-BHO-akc-d-12-0-UI"
/clone="UI-M-BHO-akc-d-12-0-UI"
/dev stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/clone lib="NIH BMAP M SI"
/clone lib="nut is a subtracted library derived fro normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hipoccampus). The driver used for subtraction consisted of a pool of 20,000 cDMA clones obtained from non-normalized and normalized libraries of these ten regions of the mouse brain.
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                                                                                                                                                                            Score 473.8; DB 9;
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Email: genome resegec.riken.go.jp,

URL:http://genome.gsc.riken.go.jp,

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,

Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

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wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,

watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,

Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira and Hayashizaki,Y.,

and Hayashizaki,Y.,

RIKEN integrated sequence analysis (RISA) system-384-format
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                                                                                                                                                                                                                                                                                                                                              Laboratory for Genome Exploration Research Group, RIKEN Genom
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BB703259 RIKEN full-length enriched, in vitro fertilized eggs Mus musculus cDNA clone 7420449J15 3', mRNA sequence.

BB703259
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Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2001)
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KONDO,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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                                  GAAAACGTTTCTGCTAGATGGGGCTAATGGAATGGACAAGTGAGCTTTCTCCCCTCTTCA
                                                                                                                  GGACAAACGCCTGTCCTGCGACAGCACCTTCAGCTTCAAATACATCATTTAGTGAGAGTC 1122
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                                                                                                                                                             CAGACTTCGCCACGTGGACCCTAAACGCCCCCATCGGCAAGACTTGTGTGGGAGATGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fertilized eggs"

[note "Site 1: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research In Riken RIKEN. Division of Experimental Animal Research Was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGGAGCCAAGAGCTCTTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissue type="in vitro fertilized eggs" dev_stage="egg"
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98.2%;
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Pred. No. 8.8e-58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10;
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninoi,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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Watshiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
and Hayashizaki,Y.
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Mus musculus (house mouse)

Mus musculus

Bukaryota; Metazoa; Chordata;

Bukaryota; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K.,
Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,
Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N.,
Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
Muramatsu,M. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                         RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Re 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory for Genome Exploration Research Group Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanaga Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2001)
Contact: Yoshihide
                                                                                                                                                                                                                                                                                   Please visit our web further details.
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                                                                          /db_xref="taxon:10090"
/clone="7420466L07"
                                                                                                                            /strain="C57BL/6J"
/tissue_type="in vitro fertilized
/dev_stage="egg"
                                                       /sex="female"
                                                                                                                                                                                organism="Mus musculus"
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Sciurognathi; Muridae;
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 Eukaryota, Metazoa, Chordata,
                                 Mus musculus (house mouse)
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                                                                                              Mouse sixteen-cell-embryo 3', mRNA sequence.
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/clone_lib="RIKEN full-length enriched, in vitro
fertilized_eggs"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
                                                                  GI:3979844
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Pred. No. 1.4e-52;
0; Mismatches 32;
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Craniata; Vertebrata;
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musculus cDNA clone 7420484F16 3', mRNA
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EST.
 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                        Mus musculus (house mouse)
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ERATO/Doi Project at Wa
Unpublished (1998)
Contact: Hirofumi Doi
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Ko,M.S.H., Kitchen,J.R., Wang,X., Threat,T.A., S
Depalma,G.B., Liang,Y., Kargul,G.J., Sharara,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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/dev_stage="sixteen-cell-embryo"
/clone_lib="Mouse sixteen-cell-embryo cDNA"
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/mol_type="mRNA"
/strain="C57BL/6J"
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/clone="J0917G09"
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
wastahiki,M., Yoneda,Y., Ishikawa,T., Okazak,K., Tanaka,T.,
Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
and Hayashizaki,Y.
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Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,
Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K.,
Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M.,
Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R.,
Okazaki, Y., Okido, T., Salto, R., Sakai, C., Sakai, K., Sakazume, N.,
Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Takahashi, F., Takaku-Akahira, S.,
Nuramaka T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A.,
Muramateu, M., and Hayashizaki, Y.,
Tituru T., Toyara, Matahiki, A., Yasunishi, A.,
Muramateu, M., and Hayashizaki, Y.,
Tituru T., Takaka, T., Takaka, T., Takaka, T., Takaka, T., Takaka, T., Tomaru, A., Takahira, S.,
Muramateu, M., and Hayashizaki, Y.,
Tituru T., Takaka, T., Tomaru, A., Takaka, T., Takaka, T., Takaka, T., Takaka, T., Takaka, T., Tomaru, A., Takaka, T., T
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Laboratory for Genome Exploration Research Group, RIKEN Genom
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-Cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045,
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Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      further details.
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Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
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81-45-503-9222
                                                                                                                                                                                   /clone_lib="RIKEN full-length enriched, in vitro fertilized eggs"
/note-"Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                      tissues.
                                          /tissue_type="in vitro fertilized eggs"
/dev_stage="egg"
/lab_host="DH10B"
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/db_xref="taxon:10090"
/clone="7420484F16"
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                                                                                                                                                                                       Doi Bioasymmetry Project, ERATO
Japan Science and Technology Corporation (JST)
WBG Marive East 12F, 2-6 Nakase, Mihama-ku, Ct
                                                                                                                                                                                                                                       Unpublished (1998)
Contact: Hirofumi Doi
                                                                                                                                                                                                                                                                                 KO,M.S.H, Kitchen,J.R., Wang,X., Threat,T.A., Sun,T., DePalma,G.E., Liang,Y., Kargul,G.J., Sharara,R. and Doi,H.
Systematic analyses of genes expressed in unfertilized mouse eggs (The ERATO/Doi Project at Wayne State University) (Ko,M.S.H. et
                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                            hd@bioa.jst.go.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse unfertilized egg cDNA Mus musculus cDNA clone 3^{\prime}, mRNA sequence.
                                           /dev_stage="unfertilized egg"
/clone_lib="Mouse unfertilized
                                                                      /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="J0426F07"
                                                                                                                                                                                                                                                                                                                                               Eutheria; Rodentia;
1 to 590)
                                                                                                                                 organism="Mus musculus"
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Pred. No. 3.1e-50;
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Tel: 301 443 1706

Pax: 301 443 9890

Email: mEST@mail.nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH SENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be non-redundant arrays of BMAP cDNAs whose availability will be
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                                                                                                                                                                                                                                                                           Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda,
20892-9643, USA
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UI-M-BH3-awu-b-08-0-UI.sl NIH BMAP M S4 Mus musculus
UI-M-BH3-awu-b-08-0-UI 3', mRNA sequence.
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1 (bases 1 to 450)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                crercaaccccereeccaceccececeeaaaa 396
                                                      CTGTCAACCCCGTGGNCACGCCGGCGCGCCGGAGA 450
                                                                                                                                                                           CAGCCGTGACGCTGCGGTGCAGGTGAACCCGCGCGCGACGCCTCGGTGCAGTGTTCACT
                                                                                                                                                                                                                                                                                      CAGCCGTGACGCTGCGGTGCAGGTGAACCCGCGCGCGACGCCTCGGTGCAGTGTTCACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /Clone 1D="MIH_BMAP M S4"
//Other="Vector: pT713D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The NH BMAP M S4 library is a subtracted library of a series, ultimately derived from a mixture of individually tagged normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hipoccampus) after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries were generated in this process: NIH_BMAP_M_S4, NIH_BMAP_M_S3.3, NIH_BMAP_M_S4, NIH_BMAP_M_S4, NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.1, Clones from which 3' ESTS had been derived was used as a driver in a hybridization with a pool of the NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.3, N
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/lab_host="DH10B (Life Technologies)"
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Pred. No. 1.9e-49;
0; Mismatches 1;
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JOURNAL COMMENT
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URL:http://genome-gsc.riken.go.jp,
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further detalls.
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B Akimura, T. Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konmo, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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419 bp mRNA linear EST 1
BB704449 RIKEN full-length enriched, in vitro fertilized
musculus cDNA clone 7420464A04 3', mRNA sequence.
BB704449
BB704449.1 GI:16053284
EST.
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81-45-503-9216
fertill zee eggs"

fertil zee eggs"

fnote="Site 1: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                        sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="7420464A04"
                                                                                                                                                                                                                                                                                         sue_type="in vitro fertilized
stage="egg"
_host="DH10B"
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Encyclopedia of Mouse

(Akimura,

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          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 521)

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Pred. No. 2.5e-49;
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URL:http://genome.gsc.riken.go.jp,

URL:http://genome.gsc.riken.go.jp,

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Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

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watshiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,

watshiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,

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Sugahara,Y. and Hayashizaki,Y.

Computer-based methods for the mouse full-length cDNA

computer-based methods for the mouse full-length cDNA
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Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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                                                     CAGTTCTTAGAGCAGAAG-TACGGCTACTATCACTGCAAGGACTGCAAAATCCGGTGGGA 857
                                                                                                                    GCCCCGCGGACCAGCCGCTCCCCCAAACCACGGAGCAGGACAAGGGGCACCGGCGTTTC
                                                                                                                                                                               GCCCCTCGAGACCAGGCCTCCCCGCAAAGCACGGAGCAGGACAAGGAGCGCCTGCGTTTC 798
CAGTTCTTAGAGCAGAAGTTACGGGTAGTATCACAGCAAGGAC-GCAAAATCCGATGGGA 130
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fertilized eggs"
/note="Site 1: Sall; Site 2: BamHI; cDNA library was
/note="Site 1: Sall; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
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                                                                                                                                                                                                                                        28.8%; Score 367.4; DB 10; Length 521; 87.3%; Pred. No. 1.2e-45; tive 0; Mismatches 61; Indels 4;
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B58 GAGGGCCTATGTGTGTGTGTGCAGGGCACCAGTAAGGTGTACATCAAACAGTTCTGCC 917 131 GAGGGGCCTATGTGTGTGTGTGTGCAGGCACCACTAAGGTGTACTTCAAACAATCTTGCGC 190 918 GAGTGTGTGAGAAATCCTACAACCCTTACAAGGTGGAGGACATCACCTGTCAAAGGTTGTA 977
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TRAAGGTGTTACTTCAAACAGTTCTGCC TAAAATTCTTCTGCCGC TRGAAGGACATCACCTGTCAAAGTTGTA
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Search completed: April 6, 2004, 20:36:04 Job time : 3705 secs

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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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1277
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AY191415	RESULT 1
Matzuk,M.M. Zygote arrest 1 (Zarl) is a novel maternal-effect gene critical for	Wu, X., Viveiros, M.M., Eppig, J.J., Bai, Y., Fitzpatrick, S.L. and	1 (bases 1 to 1260)	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mus musculus	Mus musculus (house mouse)		AY191415.1 GI:27808689	AY191415	ulus zygote arrest 1 (Zarl)	AY191415 1260 bp mRNA linear ROD 12-MAR-2003		

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Matches 1257; Conserv
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2 (bases 1 to 1260)
Wu.X., Wang,P. and Matzuk,M.M.
Direct Submission
Submitted (04-DEC-2002) Pathology, Baseman Chara, Houston, TX 77030, USA
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     CCCGTTCTCGTCACCTTCTGTGGCCTCTCCTCACTGGAGGTTGCGGGAGGCAG
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ESAYVWCVQGTSKVYFKQFCRVCEKSYNPYRVEDITCQSCKRTRCACPVRLRHVDPKR
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motif at C-terminus"
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1 (bases 1 to 1280) Wu,X., Wang,P., Brown,C.A., Zilinski,C.A. and Zygote arrest 1 (zar1) is an evolutionarily coexpressed in vertebrate ovaries Biol. Reprod. 69 (3), 861-867 (2003)
                                                                                               Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia;
                                                                                                                                                                                  Rattus norvegicus zygote
AY283175
AY283175.1 GI:30908932
                                                                                                                                                                                                                                                                                                                                         TTCATGACAGACAGTGTTACTTGGATATAAAGCCTGTGAATAAAAGGTATTGCAAACAA 1261
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                                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                 1280 bp mRNA line
arrest 1 (Zarl) mRNA,
                                                                                                                                                                                                                                   linear
                                                   Matzuk, M.M
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Matches 1110;
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Wu, X. and Matzuk, M.M.
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GCCGAGAGAGGTGGCCGCGAGGAAAGCGGTCCCCCAGCCGCGAAGCGAGGAGGGCGATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MfpASTPHPCPHPYPTJAKKAGDGWRFGARGCRPEPPSFLPGYR CLMAAEYFDSYCAGLARATLASRMGPRPYSSRDAVQVWPRRDASVQCSLGRRTLOPGR RRASPDARPGSCQPRSPARAGRPPRSFLYSSPTAGTGGLSSSLEVAGDRQTPYKGE GRPATTGTREEPFGEVAMKAVPQRSEEGDVALAGGPGGLSSGLEVAGDRSPBARAGSPFRSBEPPGSSEEDPGSVAAMASPGSSEEDPGSVAAMASPGSEEDPGSVAAMASPGSSEEDPFAVEMAQDPSDVAASRDRASFOSTEQDKERLROFLECKYGYHCKDCNIRW SSAYVWCVQGTSKVYFKQFCRVCEKSYNPYRVEDITCQSCKRTRCACPVRLRHVDPKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="zygote arrest :
/protein_id="AAP37037.1"
/db_xref="GI:30908933"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHRODICGRCKDKRISCDSTFSFKYII"
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note="maternal factor"
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"nol_type="mRNA"
'db_xref="teaxon:10116"
'chromosome="14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene="Zar1"
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87.7%;
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Pred. No. 1.9e-189;
0; Mismatches 143;
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2 (bases 1 to 3987) Wu, X. and Matzuk, M.M. Direct Submission
                                                                                                                                                                                                                                   AY19389 3987 bp I
AY19389 AY193889 GI:27808699
                                                                      the oocyte-to-embryo transition Nat. Genet. 33 (2), 187-191 (20
                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 3987)
                                                                                                                                                                                         Mus musculus (house mouse)
                                                                                                    Zygote arrest 1 (Zar1) is a novel maternal-effect
                                                                                                                                  ₩u, X.,
                                             .2539046
                                                                                                                                                                                                                                                                                                                                                         AAACA 1262
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                                                                                                                                  Viveiros, M.M.,
                                                                                                                                Eppig, J.J.,
                                                                                                                                                           Craniata; Vert
Sciurognathi;
                                                                                                                                  Bai,Y.,
                                                                                                                                                                                                                                                                 ONA linear ROD gene, complete cds.
                                                                                                                                                               Vertebrata;
thi; Muridae;
                                                                                                                                  Fitzpatrick, S.L.
                                                                                                                                                               Euteleostomi; 
; Murinae; Mus
                                                                                                       critical
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On Jan 21, 2003 this sequence version replaced gi:27808693
Location/Qualifiers
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(bases 1 to 3987)
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/gene="Zar1"
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/mol_type="genomic DNA"
/strain="129/SvEv"
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TX 77030, USA
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Mus musculus (house mouse)

Mus.

HTG; HTGS_PHASE1; HTGS_DRAFT. unordered pieces. AC122733 AC122733.2 GI:28195556 AC122733 147464 bp Mus musculus clone RP24-506B15, WORKING linear HTG 02-FEB-2003 DRAFT SEQUENCE, 21

CE 2 (bases 1 to 147464)

RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Camarata, J., Campopiano, A., Chang, J., Charg, J., Charg, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreita, P., FitzGerald, M., FitzHugh, W., Gage, D., Faro, S., Ferreita, P., FitzGerald, M., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacClean, C., Macdonald, P., Major, J., Marquis, N., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norman, C., MacCarthy, M., McEwan, R., McKernan, K., Meldrim, J., O'Connell, P., O'Norman, C., Norman, C., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Travers, M., Unpublished Mus musculus, clone RP24-506B15 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 147464) Birren, B., Nusbaum, C. and Lander, E.

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Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C.,
Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,
Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J.,
Myuyen, C., Nicol, R., Norbu, C., O'Conner, T., O'Donnell, P.,
O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C.,
Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,
Vyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (02-FRB-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 2, 2003 this sequence version replaced gi:21206317.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
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Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
Lindblad Toh,K., Liu,G., Lui,A., Mabbitt,R., MacLean,C.,
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                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence gas soon as it is available and the accession number will
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Matches 800; Conservative
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Contact: humquery@sanger.ac.uk
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                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                          /clone="RP23-384C22"
/clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
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Mouse DNA sequence from clone RP23-384C22 on chromosome
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complete
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Bukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

--- Genome Center

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMEL; Sw.; SWISSPROT; TT:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-384C22 is from the RPCI-23 Mouse PAC library constructed by the group of Pieter de Jong.

For further details see http://www.chori.org/bacpac/home.htm

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality = 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.

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/db_xref="taxon:10090" /chromosome="X"

Score 799.4; DB 10 Pred. No. 1.1e-155; 0; Mismatches 1; DB 10; Indels Length 200535; 0; Gaps

0

TCCTTATCCGCAGGCCACCAAAGCCCGGGGATGGCTGGAGGTTCGGAGGCCCAGGGGCTGCCG GGCGGGCGAGGCGCGGACCCCATGTTCCCCGGCGAGCACGTTCCACCCCTGCCCGCA GGCGGGCGAGGCGCGGACGCACCCCATGTTCCCGGCGAGCACGTTCCACCCCTGCCCGCA 182 131302 122 131243

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                                                                                                                                                                                                                                            Birren, B., Nusbaum, C. and Lander, Mus musculus chromosome 5, clone
                                                                                                                                                                                                                                                                                                                                                                                        AC107686.3 GI:38424195
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP
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COMMENT

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CB 3 (bases 1 to 168073)

RS Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderon, B., Musbaum, C., Lander, E., Barna, N., Bastien, V., Bloom, T., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Barderon, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslawkiy, L., Boukhgalter, B., Cammarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodey, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagoopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Ilagoopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Ilados, T., Levine, R., Kamata, A., Karatas, A., Kells, C., Landers, T., Levine, R., Kamata, A., Karatas, A., Kells, C., Landers, T., Levine, R., Kamata, R., Kalls, C., MacCarthy, M., MacGanald, P., Major, J., Manning, J., Matthews, C., MucCarthy, M., MacGanald, P., Major, J., Manning, J., Matthews, C., Murphy, T., Naylor, J., MacGarthy, M., Murphy, T., Naylor, J., MacGarthy, M., MacCarthy, M., Oliver, J., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nacubas, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Mihova, T., Stubhs, M., Sepencer, B., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that h provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and by the finished sequence as soon as it is available and the submittor.
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Web site: http://www-seq.wi.mit.edu
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                                                                                                                                                                 CAGCCGTGACGCTGCGGTGCAGGTGAACCCGCGCGCGACGCCTCGGTGCAGTGTTCACT
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45922. .100777
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vector_side:left"
3492. .11221
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20272. .45821
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clone_end:T7
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143570. .168073
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100878. .143469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="assembly_fragment
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clone_lib="RPCI-24 Male Mouse
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11221: contig of 7730 bp in length
11221: gap of 100 bp
11321: gap of 100 bp
20171: contig of 8850 bp in length
20171: gap of 100 bp
45821: contig of 25550 bp in length
45921: gap of 100 bp
100777: contig of 54856 bp in length
100877; gap of 100 bp
143669: gap of 100 bp
143669: contig of 42592 bp in length
143669: contig of 42592 bp in length
143669: contig of 42594 bp in length
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Pred. No. 6.7e-133;
0; Mismatches 22;
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RRS Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Badwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buthay, C., Burch, P., Burrell, K., Caderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Cchen, R., Chen, Y., Chen, Z., Chu, J., Clacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chavez, D., Deramo, C., Ding, Y., Dinh, H., Divya, K., Davila, M.L., Davis, C., Davy-carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Dirbin, K., Duval, B., Baves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Perrandez, S., Finley, M., Flaggy, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregorgis, S., Geer, K., Gill, R., Garcia, A., Garner, T., Garza, M., Gebregorgis, S., Geer, K., Gill, R., Garcia, A., Garner, T., Garza, M., Gebregorgis, S., Geer, K., Gill, R., Garcia, A., Garner, T., Garza, M., Gunaratne, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, S., Hladun, S.L., Hodgson, A., Hogues, M., Guevra, W., Gunaratne, P., Havlak, P., Hayes, A., Henderson, N., Hernandez, J., Jackson, A., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kovis, C., Liu, J., Mandhoud, M., Malloy, K., Mangum, A., Mangum, B., Mapu, P., Martin, K., Martin, R., Martinez, E., Montemayor, J., Moore, S., Mair, L., Mandhoud, M., Mallosavi, J., Mair, L., Mair, L., Mair, L., Mair, L., 
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HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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Rattus norvegicus clone CH230-159N5, WORKING DRAFT SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGAGCTCCTGCGTTTCCAGGT 64233
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Direct Submission

Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 20, 2002 this sequence version replaced gi:23195602.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (06-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat Genome Sequencing Consortium.
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                                                            NOTE: Estimated insert size may differ from sequence length (see http://www.hggsc.bcm.tmc.edu/docs/Genbank draft_data.h NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
by the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                          Center project name: GZCZ
Center clone name: CH230-159N5
Center clone name: CH230-159N5
Center clone name: CH230-159N5
Center clone name: Phrap; version 0.990329
Assembly program: Phrap; version 0.990329
Consensus quality: 216235 bases at least Q40
Consensus quality: 218057 bases at least Q20
Consensus quality: 219408 bases at least Q20
Estimated insert size: 221324; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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Web site: http://www.hgsc.bcm.tmc.
Contact: hgsc-help@bcm.tmc.edu
Center Troject Information
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REFERENCE AUTHORS

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Matches 708;
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/mol_type="genomic DNA"
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             Egan, A., Escotto, M., Eugens, C., Evans, C.A., Falls, T., Fan, G., Egan, A., Escotto, M., Eugens, C., Evans, C.A., Foster, M., Gerraguez, G., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebragecorgis, E., Geer, K., Gill, R., Gardy, M., Guerra, M., Guevara, W., Gunaratne, P., Haaland, W., Hamilton, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, A., Hodgson, A., Hogues, M., Hellins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Karpathy, S., Kelly, S., Kelly, S., Kally, S., Khan, Z., King, L., Kovar, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, S., Kelly, S., Kally, S., Kang, L., Kovar, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Joulseged, H., Lozado, R.J., Lu, X., Ma, J., Mansuhaey, S., Mcleod, M.P., Mcleod, M.P., Mortis, S., Martin, R., Perez, A., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Popovic, D., Primus, E., Neut, J., Reigh, R., Reilly, M., Reigh, R., Reiter, M., Richards, S., Raigs, F., Rilly, R., Reigh, R., Soa, J., Sheet, M., Siecol, A., Siecol, A., Siecol, J., Sitter, C.D., Smajs, D., Shet, H., Shen, H.,
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Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Cyle, M., Cree, A., D'Souza, L.,
Davila, M.L., Davis, C., Davis, C., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Eggan, A., Escotto, M., Flagg, N., Farler, M., Forter, M., Forter, M., Forter, D.,
Finley, M., Flagg, N., Forter, M., Forter, M., Forter, D., Forter, M., Forter, D., Forter, M., Forter,
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HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC125993 237695 bp Di
Rattus norvegicus clone CH230-74L11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA linear HTG 10-MAY-2003

1, *** SEQUENCING IN PROGRESS
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JOURNAL
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misc_feature
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On May 10, 2003 this sequence version replaced gi:23096451.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome spansors are contigs will be indicated in the feature
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Direct Submission
Submitted (02-UUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 237695)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 237695: contig of 237695 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.)
NOTE: This is a 'working draft' sequence. It currently consists of I contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: GGIZ

Center clone name: CH230-74L11

Center clone name: CH230-74L11

Center clone name: CH230-74L11

Center clone name: CH230-74L11

Center clone name: Atlas 3.0;

Assembly program: Atlas 3.0;

Consensus quality: 23641 bases at least Q40

Consensus quality: 231444 bases at least Q30

Consensus quality: 231444 bases at least Q20

Consensus quality: 232679 bases at least Q20

Estimated insert size: 242796; sum-of-contigs estimation

Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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Contact: hgsc-help@bcm.tmc.edu
------ Project Information
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                                                                                                                                                                                                              /note="wgs_end_extension clone_end:T7" complement(5394. 6172)
end_sequence:BH339391"
complement(234275. .235086)
                                                                                                                                /note="clone_boundary clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10116"
/clone="CH230-74L11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Rattus norvegicus"
/mol_type="genomic DNA"
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  AC127083 262139 bp
Rattus norvegicus clone CH230-69F8,
4 unordered pieces.
AC127083
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                                                                                                                                                                                             GGACCCCGGTGATTCGGATGCCCCTCGAGACCAGGCCTCCCCGCAAAGCACGGAGCAGGA
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clone_end:Sp6
site:EcoRI
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Pred. No. 4.6e-120;
0; Mismatches 90;
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SEQUENCING
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IN PROGRESS ***,
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KEYWORDS
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AUTHORS
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AUTHORS
                 COMMENT
Submitted (20-NOV-2002) Human Genome Sequencing Center, Departmen of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 6, 2002 this sequence version replaced gi:23269432.
The sequence in this assembly is a combination of BAC based reads
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Anjelb. C., Mallen, H., Alsbrooks, S., Amill, A., Anguland, D., Anjyalbechil, V., Apoyagi, A., Pyodeji, M., Baca, E., Baden, H., Baldwin, D., Bandarnanke, D., Barber, M., Barristead, M., Benahmed, F., Biswalo, K., Balat, J., Blankenburg, K., Blith, P., Brown, M., Bhay, C., Burch, P., Burrell, K., Caleron, E., Chu, J., Carcenas, V., Carter, K., Cavazos, I., Cease, H., Center, A., Chu, J., Chako, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, C., Devoland, C., Deckell, R., Cox, C., Cyle, M., Cree, A., D'Souza, L., Davila, M., Davis, C., Davy, Carroll, L., De Juda, H., Divor, K., Deraber, H., Began, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernadez, S., Finley, M., Faleg, M., Forbes, L., Foster, M., Guevara, M., Gurarene, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harrey, Y., Havak, P., Hawes, A., Henderson, M., Hernandez, J., Harrey, Y., Havak, P., Hawes, A., Henderson, M., Hernandez, J., Harrey, Y., Havak, P., Hawes, A., Handerson, M., Hernandez, J., Lu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lozes, M., Vangum, B., Wague, P., Martin, K., Martin, R., Martinez, D., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, X., Mangum, A., Mansheshwari, M., Wahindarthe, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, M., Martin, R., Martin, R., Martinez, S., Mangum, P., Martin, K., Martin, R., Martinez, P., Pazo, M., Okaro, J., Pazo, M., Pazo, M., Pazo, M., Saroy, G., Scott, G., Shateman, S., Shen, H., Sh
Submitted (13-JUL-2002) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 262139) Rat Genome Sequencing Consortium.
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                         Worley, K.C.
Direct Submission
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Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Center, Department of Medicine, One

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Best Local Sim:
Matches 708;
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                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/cenbank draft data.html).

NOTE: This is a "working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
                                                                                                   TCCTTATCCGC---AGGCCACAAAGCCGGGGATGGCTGGAGGTTCGGAGGCCAGGGGCTG 119
                                                         TCCTTACCCGCCCACGGCAGCCAAAGCCGGGGATGGCTGCAGGTTTGGAGCCAGGGGCTG 237212
                                                                                                                                                                                                                              GGCGGGCGAGGCGCGGGACGCACCCATGTTCCCGGCGAGCACGTTCCACCCCTGCCCGCA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as soon as it is available be preserved.
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------ Summary Statistics
Assembly program: Phrap, version 0.990329
Consensus quality: 200303 bases at least Q40
Consensus quality: 206134 bases at least Q20
Consensus quality: 20510 bases at least Q20
Consensus quality: 209370 bases at least Q20
Consensus quality: 209370 bases at least Q20
Consensus quality: 209370 bases at least Q20
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                                                                                                                                                                                                                                                                                    Conservative
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563 4662: gap of unknown length
663 259056: contig of 254394 bp in length
057 259156: gap of unknown length
157 260299: contig of 1143 bp in length
300 260399: gap of unknown length
400 262139: contig of 1740 bp in length
Location/Qualifiers
1 262139
                                                                                                                                                                                                                                                                                                                                                                                                                   /note="wgs_contig"
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|72942. .174088
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08494. .109772
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88.1%;
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ylor College of Medicine
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                                                                                                                                                                                                                                                                              Score 628; DB 2;
Pred. No. 4.6e-120;
0; Mismatches 90;
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Kamar, A., Karstes, A., Kalis, C., LaRocque, K., Lamazares, R., Ladders, T., Laboczky, T., Lawinas, R., Liulo, M., Machamid, P., Major, J., Marquis, N., Matthaws, C., McCarthy, M., McC
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/clone="RP23-300K5"
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Zygote arrest 1 (Zar1) is a novel maternal-effect the occyte-to-embryo transition
Nat. Genet. 33 (2), 187-191 (2003)
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Direct Submission
Submitted (04-DEC-2002) Pathology, B.
Baylor Plaza, Houston, TX 77030, USA
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Wu,X., Viveiros,M.M., Eppig,J.J., Bai,Y., Fitzpatrick,S.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                             CECCCECAGGGCAGCTGCGACGTGGCGGTGCAGGTGAGCCCGCGCATCGACGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCGAGGCCTGGAGCAGGGCAGCCCCCAGAACGGCGCCCCGCGGCCCATGCGCTTCCCGCG
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                                                                                                                                GGCCGGCCCGGGGCCGAGGGCACCACGGGTGGCGGCTCTTTCTCCCAGCAGCCATCCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="ZAR1"
/codon_start=1
/product="zygote arrest 1"
/protein_id="AA024707.1"
/db_xref="GI:27808692"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MAALGDEVLDGYVFPACPPCSYRYPYPAATKGKGAAGGSWQQRG
RGCLPASSPCSAGAAGGSWQQRG
SCDVAVQVSFRIDAAVQCSGLGRRTTAAEYFPSXQRERLMALLAQVGFOGLGFRARRAG
SCDVAVQVSFRIDAAVQCSGLGRRTTQFRARDFESPAGFGAEGTTGGGSFSQQPSRRGL
EQGSPQNGAFRFMRFPRTVAVYSPLALRRLTAFLEGFOFDAAGGQRSGASDGERGPPPA
RLQGSEEGEVWTKKAPRRPQSDDDGEAQAAVRASWEQPADGFELFPREAQEGEAAPRS
RLQGSEEGEVWTKKAPRRPQSDDDGEAQAAVRASWEQPADGFELFPREAQEGEAAPRS
RLRSFGQPPSAGRARDGGDGREAAVAGGESPNSPELGKERLFQFLEQKYGYYHCKD
CNIRWESAYWCVQGTWKYPEYQFCETCQKSYNPYRVEDITCQSCKQTRCSCFVKLRH
VDPKRPHRQDLCGRCKGKRLSCDSTFSFKYII"
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mol_type="mRNA"

db_xref="taxon:9606".

chromosome="4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              map="4p12"
                                                                                 --TGTCAACCCCGTGGCCACGCCGGCGCGCGAGATCCCCGCGATCCTGGCA
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Pred. No. 1e-62;
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AC108848/c
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2 (Dases 1 to 212848)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Bartien,V., Boguslavkty,L., Boukhgalter,B.
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
                                                                                                                               Eukaryota; Metazoa; Chordata; (Mammalia; Eutheria; Rodentia; 1 (bases 1 to 212848)
Birren,B., Linton,L., Nusbaum, (Mushuseulus, clone RP23-300K5
                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                            AC108848.2 GI:20336129
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP
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                                                                                                                                                                     'n
                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                     and Lander,
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Chosepal Y. Colargalo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Darbellano, K., Dewark, Chiar, J.S., Dodge, S., Paro, S., Perretari, P., Pitchigh, W., Gage, D., Galagan, J., Gardd-Paere, M., Gard, P., Cardd-Paere, M., Gard, P., Kardd-Paere, M., Gard, M., Cardd-Paere, M., Cardd-Paere,
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is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

641: contig of 641 bp in length
642: 741: gap of 100 bp
127: contig of 686 bp in length
1428: 1527: gap of 100 bp
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Direct Submission
Submitted (24-APR-2003) Pathology, Be
Submitted Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus laevis (African clawed frog)
Xenopus laevis
Xenopus laevis
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibba; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 1052)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopus laevis zygote arrest 1 (Zarl) mRNA, X283176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wu,X., Wang,P., Brown,C.A., Zilinski,C.A. and Matzuk,M.M. Zygote arrest 1 (zarl) is an evolutionarily conserved gen expressed in vertebrate ovaries Biol. Reprod. 69 (3), 861-867 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AY283176.1 GI:30908934
CTTCAAATACATCATTT 1112
                                                                                                                                                            TAAAAGAACTAGATGTGCCTGCCCAGTCAGATTTCGCCACGTGGACCCTAAACGCCCCA
                                                                                                                                                                                                     CAGGACATGTCAGAAATCCTATAATCCCTACCGTGTGGAAGACATCATGTGTCAGAGCTG
                                                                                                                                                                                                                                                                          GAGAGCGCCTACGTGTGGTGTGCAGGAAACCAATAAGGTG-TACTTCAAGCAGTTCTG
                                                                                                                                                                                                                                                                                                         GAGAGCGCCTATGTGTGGTGTGTGCAGGGCACCAGTAAGGTGTTACTTCAAACAGTTCTG
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                                                                                          TCGGCAAGACTTGTGTGGGAGATGCAAGGACAAACGCCTGTCCTGCGACACCACCTTCAG 1095
                                                                                                                                                                                                                                   CCGAGTGTGAGAAATCCTACAACCCTTACAGAGTGGAGGACATCACCTGTCAAAGTTG
                                                                                                                                                                                                                                                                                                                                                                                    TTCCAGTTCTTAGAGCAGAAGTACGGCTACTATCACTGCAAGGACTGCAAAATCCGGTGG
                                                                                                                               CAAGCAGACGAGATGCGCGTGTCCTGTCAAACTGCGTCACGTTGACCCCAAGAGGCCCCCA
                                                                                                                                                                                                                                                                                                                                                 TTCCAGTTCCTGGAGCAGAAGTACGGATATTATCACTGTAAGGACTGCAACATCCGCTGG
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X. and Matzuk, M.M.
                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
/product="zygote arrest 1"
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PEQGSPASPTKTVRFPRTIAVYSPVAAGRLAPFQDEGVNLEEKGEAVRSEGSEGGRQE
GKQGDCSIKEQWKMDKTDEEBAAPAQTRPKFQFLEQKKGYYHCKDCNIIWESAYVWCV
QEINKYYFKQFCRTCQKSYNPYRVEDIMCQSCKQTRCACPVKLRHVDPKRPHRQDLCG
RCKGKRLSCDSTFSFKYII"
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mol_type="mRNA"
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Pred. No. 2.4e-32;
0; Mismatches 62;
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AY283177
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DEFINITION
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Best Local (
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                                                                                                                                                                                     896
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                                                                                                                                                                                                                                                            836
                                                                                                                                                                                                                                                                                                626 AGGGCAAAGCGCGTGTCCGCTTCCAGTTTCTGGAACAGAAGTACGGCTACTATCACTGCA
                                                                                                                                                                                                                                                                                                                                      776
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                                                                                                                                                                                                                                                                                                                                                                          255;
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Submitted (24-APR-2003) Pathology, Baylor
Submitted (Plaza, Houston, TX 77030, USA
Baylor Plaza, Houston, TX 77030, USA
Location/Qualifiers
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Wu, X. and Matzuk, M.M.
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Wu, X., Parest, P. Brown, C.A., Zilinski, C.A. and Matzuk, M.M.
Zygote arrest 1 (zarl) is an evolutionarily conserved gen
expressed in vertebrate ovaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takifugu rubripes (Fugu rubripes)
Takifugu rubripes
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AY283177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Actinopterygii; Neopterygii; Teleostei; Eutel
Acanthomorpha; Acanthopterygii; Percomorpha;
Tetradontoidea; Tetraodontidae; Takifugu.
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                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                      AGGACTGCAAAATCCGGTGGGAGAGCGCCTATGTGTGGTGTGTGCAGGGCACCAGTAAGG
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                       GTGGACCCTAAACGCCCCCATCGGCAAGACTTGTGTGGGAGATGCAAGGACAAACGCCTG
                                                                       GACATCACATGTCACGTATGCAACAAGGCCCGCTGTGCCTGCGCAGAAACGCAGCGCCAC
GTTGACCCAAAGAGGCCCCACAGGCAGGACCTGTGCGGCAGGTGCAAGGGGCAAGCGGCTG
                                                                                                   T-TTACTTCAAGCAGTTCTGTAGGAAATGCCAAAAAGACTTTAACCCCGTACCGCGTAGAG
                                                                                                                                                                                   TGTTACTTCAAACAGTTCTGCCGAGTGTGTGAGAAATCCTACAACCCTTACAGAGTGGAG
                                                                                                                                                                                                                           GAGAATGCAACCTGCGATGGGAGAGCGCGTACGTTTGGTGCGTTCAGGGCACTAACAAGG
                                                                                                                                                                                                                                                                                                                                    AGGACAAGGAGCGCCTGCGTTTCCAGTTCTTAGAGCAGAAGTACGGCTACTATCACTGCA 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTCAAGTATATCATTT
                                                                                                                                                                                                                                                                                                                                                                      15.3%; Score 194.8; DB 5; Larity 75.4%; Pred. No. 4.7e-30; Conservative 0; Mismatches 82;
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LEQKYGYYHCRECNLRWESAYVWCYQGTNKVYFKQFCRKCQKDFNPYRVEDITCHVCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KARCACAETQRHVDFKRPHRQDLCGRCKGKRLSCDSTFSFKYIV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Takifugu rubripes"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="maternal
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Euteleostei; Neoteleostei;
rpha; Tetraodontiformes;
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Best Local Similarity
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1014 ACGTGGACCCTAAACGCCCCCATCGGCAAGACTTGTGTGGGAGATGCAAGGACAAACGCC 107:
                                    871
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Danio rerio zygote arrest 1 (zar1) mRNA, complete
AY283178
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (24-APR-2003) Pathology, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wu, X. and Matzuk, M.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wu,X., Wang,P., Brown,C.A., Zilinski,C.A. and Matzuk,M.M. Zygote arrest I (zarl) is an evolutionarily conserved gene expressed in vertebrate ovaries expressed in vertebrate 70 areas (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes, Cyprinidae, Danio.

1 (bases 1 to 1084)
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Danio rerio
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                                                                                                                                 GGTGTTACTTCAAACAGTTCTGCCGAGTGTGTGAGAAATCCTTACAACCCTTACAGAGTGG 953
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                                                                   AGGACATCACCTGTCAAAGTTGTAAAAGAACTAGATGTGCCCTGCCCAGTCAGATTTCGCC 1013
                                                                                                                                                                                                                                                 GAAGTCCAAGGCTCGTGAGATTTCAGTCTTTGGAGCAGAAGTATGGATTCTATCATTG
                                                                                                        GGT-TTATTTCAAGCAGTTCTGCAGAACATGCCAGAAATCATTCAACCCATACCGGGTTG
                                AGGACATAGCATGTCAGACTTGCAAGAAAGCTCGCTGCACATGTTCTGTCAAGTCGCGTC
                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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                                                                                                                                                                                                                                                                                                                    Score 194.6; DB 5;
Pred. No. 5.2e-30;
0; Mismatches 84;
                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                       Length 1084;
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	В	Š	дb
	991 TGTCCTGCGACAGCACGTTCAGCTTCAAGTACATCTAG 1031	1074 TGTCCTGCGACAGCACCTTCAGCTTCAAATACATCATTTAG 1114	931 ACGTGGACCCCAAAAGACCCCATCGGCAGGATCTGTGCGGCCGCTGTAAAGGCAAGCGTC 990

Search completed: April 6, 2004, 19:34:21 Job time : 5131 secs

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Result
No.
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Maximum DB seq length: 200000000
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Perfect score:
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Match
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Maximum Match 100%
Listing first 45 summaries
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US-09-844-864-29

US-09-844-864-23

US-09-844-864-23

US-09-844-864-23

US-10-844-864-23

US-10-844-864-20

US-10-10-848-8468-1

US-10-084-8468-99

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Sequence 22, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 25, Appl
Sequence 23, Appl
Sequence 20, Appl
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Sequence 1879, App
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   Conservative
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100.0%; Pred. No. 0;
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APPLICANT: Matzuk, Martin
APPLICANT: Men, Yongsheng
APPLICANT: Wen, Yongsheng
APPLICANT: Wen, Xuemei
TITLE OF INVENTION: OVARY SPECIFIC GENES AND PROTEINS
FILE REPERENCE: P01925US2 / 09807797 / OTA 99-48
CURRENT APPLICATION NUMBER: US/09/844,864
CURRENT FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: 60/106,020
PRIOR APPLICATION NUMBER: 60/106,020
PRIOR FILING DATE: 1998-10-28
PRIOR FILING DATE: 1998-10-28
NUMBER: OF SEQ ID NOS: 25
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                                                                                                        CATCCTTATCCGCAGGCCACCAAAGCCGGGGATGGCTGGAGGTTCGGAGCCAGGGGCTGC
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Patent No. US20020042926A1

GENERAL INFORMATION:

APPLICANT: Matrix Martin

APPLICANT: Ren, Yongsheng

APPLICANT: Way, Xuemei

TITLE OF INVENTION: OVARY SPECIFIC GENES AND PROTEINS

FILE REFERENCE: P01925US2 / 09807797 / OTA 99-48

CURRENT APPLICATION NUMBER: US/09/844,864

CURRENT FILING DATE: 2001-04-27

PRIOR APPLICATION NUMBER: FCT/US99/25209

PRIOR APPLICATION NUMBER: PCT/US99/25209

PRIOR FILING DATE: 1998-10-28

VENTOR FILING DATE: 1999-10-28

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin version 3.0

SEQ ID NO 18

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                    GAGAGAGGTGGCCGCGAAGGAAAGCGGTCCCCCAGCCGCGAAGCGAAGGGAGGACGATGTTCA
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GAGAGAGGTGGCCGCGAGGAAAGCGGTCCCCCAGCCGCAAGCGAGGAGGGCGATGTTCA
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Pred. No. 6.2e-225;
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841 841 781 781 721 721 199 661 601 601 541 541 481 481 421 421 361 361 301

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GENERAL INFORMATION:

APPLICANT: Matzuk, Martin
APPLICANT: Ren, Yongsheng
APPLICANT: Ren, Xuemei
ITITE OF INVENTION: OVARY SPECIFIC GENES AND PROTEINS
FILE REFERENCE: P01925US2 / 09807797 / OTA 99-48
CURRENT APPLICATION NUMBER: US/09/844,864
CURRENT APPLICATION NUMBER: 60/106,020
PRIOR APPLICATION NUMBER: 60/106,020
PRIOR FILING DATE: 1998-10-28
PRIOR FILING DATE: 1999-10-28
INUMBER: OF SEG ID NOS: 25
SOFTWARE: Patentin version 3.0
SEG ID NO 22
I.EMCTER: 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LENGTH: 809
; TYPE: DNA
; ORGANISM: mus musculus
US-09-844-864-22
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US-09-844-864-22
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Best Local
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                               CTGTCAACCCCGTGGCCACGCCGCGCGCGATCCCCGCGATCCTGGCAGACCGTAGC
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Pred. No. 5e-211;
0; Mismatches 18;
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APPLICANT: Wu, Xuemei
APPLICANT: Wu, Xuemei
TITLE OF INVENTION: OVARY SPECIFIC GENES AND PROTEINS
FILE REFERENCE: P01925US2 / 09807797 / OTA 99-48
CURRENT APPLICATION NUMBER: US/09/844,864
CURRENT FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: 60/106,020
PRIOR FILING DATE: 1998-10-28
PRIOR FILING DATE: 1998-10-28
PRIOR FILING DATE: 1999-10-28
NUMBER OF SEQ ID NOS: 25
SOFTMARE: Patentin version 3.0
SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                           ; LENGTH: 305
; TYPE: DNA
; ORGANISM: mus m
US-09-844-864-21
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US-09-844-864-21
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Best Local Simi
Matches 282;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Matzuk, Martin
APPLICANT: Ren, Yongshen
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                                                                                                                                                                                                                                                                                         Similarity
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                               GCTAATGGAATGGACAAGTGAGCTTTCTCCCCCTCTCACCTCTTCCCCTTTCCAAATTCTT
                                                                                               AGCACCTTCAGCTTCAAATACATCATTTAGTGAGAGTCGAAAACGTTTCTGCTAGATGGG 1144
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                                                                AGCACCTTCAGCTTCAAATACATCATTTAGTGAGAGTACGAAACGTTTCTGCTAGATGGG
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Pred. No. 3.6e-70;
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APPLICANT: Ren, Yongsheng
APPLICANT: Wh, Xuemei
TITLE OF INVENTION: OVARY SPECIFIC GENES AND PROTEINS
FILE REFERENCE: P01925US2 / 09807797 / OTA 99-48
CURRENT APPLICATION NUMBER: US/09/844,864
CURRENT FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: 60/106,020
PRIOR FILING DATE: 1998-10-28
PRIOR FILING DATE: 1998-10-28
NUMBER: OF SEQ ID NOS: 25
SEQ ID NO 25
SEQ ID NO 25
SEQ ID NO 25
SEQ ID NO 25
APPLICANT: Ren, Yongsheng
APPLICANT: WL, Xuemei
APPLICANT: WL, Xuemei
TITLE OF INVENTION: OVARY SPECIFIC GENES AND PROTEINS
FILE REFERENCE: P01925U32 / 09807797 / CTA 99-48
CURRENT APPLICATION NUMBER: US/09/844,864
CURRENT FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: 60/106,020
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: PCT/US99/25209
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: PCT/US99/25209
PRIOR FILING DATE: 1999-10-28
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.0
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APPLICANT: Matzuk, N
APPLICANT: Ren, You
APPLICANT: Wu, Xuen
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                                                                                                                                                                                                                                                                               Sequence 19, Application US/09844864 Patent No. US20020042926A1
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TYPE: DNA
ORGANISM: mus musculus
-09-844-864-25
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APPLICANT: Ren, Y
APPLICANT: Wu, Xu
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les 266; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1106 ATCATTTAGTGAGAGTCGAAAACGTTTCTGCTAGATGGGGCTAATGGAATGGACAAGTGA 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 281
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Pred. No. 2.7e-66;
0; Mismatches 9;
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GENERAL INFORMATION:

APPLICANT: Mattuk, Martin

APPLICANT: Ren, Yongsheng

APPLICANT: Wu, Xuemei

TITLE OF INVENTION: CVARY SPECIFIC GENES AND PROTEINS

FILE REFERENCE: P01925US2 / 09807797 / OTA 99-48

CURRENT APPLICATION NUMBER: US/09/844,864

CURRENT FILING DATE: 2001-04-27

PRIOR APPLICATION NUMBER: 60/106,020

PRIOR FILING DATE: 1998-10-28

PRIOR APPLICATION NUMBER: PCT/US99/25209

PRIOR APPLICATION NUMBER: PCT/US99/25209
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APPLICANT: MATCH, Martin
APPLICANT: MATCH, Martin
APPLICANT: MACCH, Martin
APPLICANT: WL Xuemel
APPLICANT: WL Xuemel
TITLE OF INVENTION: CVARY SPECIFIC GENES AND PROTEINS
FILE REFERENCE: P01925US2 / 09807797 / OTA 99-48
CURRENT APPLICATION NUMBER: US/09/844,864
CURRENT FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: 60/106,020
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: FCT/US99/25209
PRIOR FILING DATE: 1998-10-28
VUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.0
LENGTH: 123
TYPE: DNA
OPCANTEM: MISS MISSONIES
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US-09-844-864-20
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US-09-844-864-23
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Patent No. US20020042926A1
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Best Local Similarity
Matches 100; Conserv
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Best Local Similarity 98.0%;
Matches 100; Conservative
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LENGTH: 123
TYPE: DNA
ORGANISM: mus musculus
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Patent No. US20020042926A1
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SEQ ID NOS:
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Pred. No. 7.8e-19;
0; Mismatches 2;
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US-09-844-864-24
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; TYPE: DNA
; ORGANISM: mus musculus
US-09-844-864-20
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 24
                                                                                                                                                                                                         GENERAL
                                                                                                                                                                                                                             Sequence 1133, Application US/10412699B Publication No. US20040045049A1
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Best Local Similarity
Matches 72; Conserv
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APPLICANT:
APPLICANT:
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APPLICANT: Wu, Xuemei
TITLE OF INVENTION: OVARY SPECIFIC GENES AND PROTEINS
FILE REFERENCE: PO1925US2 / 09807797 / OTA 99-48
CURRENT APPLICATION NUMBER: US/09/844,864
CURRENT FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: 60/106,020
PRIOR FILING DATE: 1998-10-8
PRIOR APPLICATION NUMBER: PCT/US99/25209
PRIOR PILING DATE: 1998-10-8
PRIOR PILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
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TYPE: DNA
ORGANISM: mus musculus
-09-844-864-24
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APPLICANT: Ren, Yongsheng
APPLICANT: Wu, Xuemei
    APPLICANT:
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                                                       Fromm, Michael E.
Heard, Jacqueline E.
Riechmann, Jose Luis
Adam, Luc J.
Broun, Pierre E.
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Pineda, Omaira
Reuber, T. Lynne
Keddie, James S.
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Pred. No. 1.7e-10;
0; Mismatches 1;
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; ORGANISM: Oryza sativa
US-10-412-699B-1133
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PRIOR FILLING DATE: 2000-03-22
PRIOR PELLOATION NUMBER: 09/533,648
PRIOR FILLING DATE: 2000-03-22
PRIOR PELLOATION NUMBER: 09/713,994
PRIOR APPLICATION NUMBER: 09/819,142
PRIOR APPLICATION NUMBER: 09/819,142
PRIOR FILLING DATE: 2001-03-27
PRIOR FILLING DATE: 2001-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 2011
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1133
LENGTH: 1500
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Best Local S
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APPLICANT: Ratcliffe, Oliver
APPLICANT: Kumimoto, Roderick
APPLICANT: Sherman, Bradley K.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: Polymucleotides and Polypeptides
FILE REFERENCE: MBI-0048CIP
CURRENT APPLICATION NUMBER: US/10/412,699B
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: 09/394,519
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PRIOR APPLICATION NUMBER: 09/489,376
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: 09/506,720
PRIOR TILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 09/533,030
PRIOR FILING DATE: 2000-03-22
PRIOR FILING DATE: 2000-03-22
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APPLICANT:
APPLICANT:
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PRIOR FILING DATE: 2000-03-22
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                                                                                                                                                                                                                                                                                                                                                                           CGGTGCAGGTGAACCCGCGCGCGACGCCTCGGTGCAGTGTTCACTCGGGCGCCGCACGC 316
                                                                                                                                                                                                                                                                                       TGCAGCCTGCAGGGTGCCGAGCCCAGCCCGACGCCCGATCGGGTTCCTGTCAACCCCGTG 376
                                                                                                                                                                                                                                                                                                                                                                                                                      AGAAGAAGCGGCGCCTCACGCCGGAGCAGGTGCATCTGCTGGAGAGGAGCTTTCGAGGAGG
                                       AGGGAGAGGGGAGCCCGGCATCCTCGGGGACCCGGGAACCGGAGCCGAGAGAGGTGGCCG
                                                                                                                                                                  GCGACTTCGACCGCCTCAAGGCGTCGTTCGACGCCCTCCGCGCCGACCACGACGCCCTCC 597
                                                                                                                                                                                                       GCCACGCCGCGCGCGAGATCCCCGCGATCCTGGCAGACCGTAGCCCCGTTCTCGTCCG 436
                                                                                                                                                                                                                                                                                                                                    AGAACAAGCTGGAGCCGGAGCGGAAGACGGAGCTGGCGCGGAAGCTAGGGCTGCAGCCGC
    AGGAGACGACGAGCGAGGGCAGCGCCGGCGCGTTGACGTCCCGGGCTTGCCTGCGG
                                                                                                                          TCCAGGACAACCACCGCCTCCACTCTCAGGTCATGTCGTTGACCGAGAAGCTGCAAGAGA
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Samaha, Raymond R.
Pilgrim, Marsha L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Creelman, Robert A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 54.2; DB 12;
Pred. No. 3.7e-05;
0; Mismatches 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      See File Wrapper or PALM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1500;
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FILL CALL

TITLE OF INVESTION: POLYMUCLECTIDES AND FOLYPEPTIDES IN PLANTS

FILE REFERENCE: MBI-0047 CIP

CURRENT APPLICATION NUMBER: US/10/374,780A

CURRENT FILING DATE: 2003-02-25

PRIOR APPLICATION NUMBER: 09/837,944

PRIOR FILING DATE: 2001-08-19

PRIOR APPLICATION NUMBER: 09/934,455

PRIOR APPLICATION NUMBER: 09/934,455

PRIOR PRIOR FILING DATE: 2001-08-22

PRIOR PRIOR APPLICATION NUMBER: 09/934,455

PRIOR APPLICATION NUMBER: 09/934,455

PRIOR APPLICATION NUMBER: 00/336,049

PRIOR APPLICATION NUMBER: 00/336,049

PRIOR APPLICATION NUMBER: 00/336,692

PRIOR APPLICATION NUMBER: 00/336,692

PRIOR FILING DATE: 2001-12-11

PRIOR APPLICATION NUMBER: 10/11,468

PRIOR FILING DATE: 2002-06-14

PRIOR APPLICATION NUMBER: 10/225,066

PRIOR APPLICATION NUMBER: 10/225,066

PRIOR APPLICATION NUMBER: 10/225,066

PRIOR APPLICATION NUMBER: 10/225,066

PRIOR APPLICATION NUMBER: 10/225,068

PRIOR APPLICATION NUMBER: 10/225,068
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US-10-374-780A-680
                                                                                                                                                                                                 , OTHER INFORMATION: Predicted polypeptide sequence is orthologous to US-10-374-780A-680
                                                                                                Query Match 4.2%;
Best Local Similarity 43.4%;
Matches 251; Conservative
                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin
SEQ ID NO 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 680, Application US/10374780A Publication No. US20040019927A1
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT: Riechmann, Jose Luis
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Heard, Jacqueline E
APPLICANT: Haake, Volker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
                                                                                                                                                                                                                                                                                                                            ENGTH: 1500
     298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reuber, 1. Reuber, 1. Reuber, James Keddie, James Pierre E
                             CCTTCCCCCCGGCTACAGACAGCTCATGGCCGCGGAGTACGTCGACAGCCACCAGCGGG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCCTGGGAGCGAGGAGCCATGTCCTGCCGCAGAGATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCGGGTGGGAGCAGCACCACCGCAGGAGGACCGGAACAGTGTGGCGGCGATGCAGTCTG
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Pilgrim, Marsha L
Dubell III, Arnold T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratcliffe, Oliver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adam, Luc J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Creelman, Robert A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pineda, Omaira
CTTCACCACCCCGACGÁGCTCCTCGAAGAGGÁGTÁCTACGÁCGAGCAGCTCCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Guo-Liang
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                                                                                                Score 54.2; DB 15;
Pred. No. 3.7e-05;
D; Mismatches 328;
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                                                                                                   Indels
                                                                                                                                           Length 1500,
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                                                                                                                                                                                                                                                                                                                 FILE REPERENCE: 1974-005
CURRENT APPLICATION NUMBER: US/10/084,846A
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: PCT/EP01/09815
PRIOR APPLICATION NUMBER: PCT/EP01/09815
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: DE 101 09 166.4
PRIOR FILING DATE: 2001-02-25
NUMBER OF SEQ ID NOS: 120
SOFTWARE: Patentin Ver. 3.2
LENGTH: 987
TYPE: DNA
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                                                                                                                                                                                              ; ORGANISM: Streptomyces viridochromogenes ; FEATURE; OTHER INFORMATION: aviG4 dna: partial sequence of coding strand 1; nucleotide ; OTHER INFORMATION: corresponds to nucleotide 45,341 of coding strand 1. US-10-084-846A-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
US-10-084-846A-99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 99, Application US/10084846A
Publication No. US20040006026A1
GENERAL INFORMATION:
APPLICANT: WEITNAUER, GABRIELE
APPLICANT: MUHLENWEG, AGNES
APPLICANT: TREFZER, AXEL
APPLICANT: BECHTHOLD, ANDREAS
TITLE OF INVENTION: AVILANYCIN DERIVATIVES
                                                                                             Query Match 4.0%;
Best Local Similarity 49.6%;
Matches 132; Conservative
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  260
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                                                GCGGCGGGAGCGCGGTGGTGGACACGGACGCGCAACTGG
  cceceercecaaceeccreecaecaccaccacaecacceccacceccacceeccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCCTGGGAGCGAGGCCATGTCCTGCCGCAGAGATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGAAGAAGCGGCGCCTCACGCCGGAGCAGGTGCATCTGCTGGAGGAGGAGCTTCGAGGAGG 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGGCGTTCGAGGAGCAGCAGCAGCAGCAGGTGAAGGCCGAGGACAGGCTGAGCACGGGCA 837
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                                                                                                Score 51.6; DB 15;
Pred. No. 0.00017;
0; Mismatches 134;
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RESULT 14
US-10-084-846A-2/c
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US-10-084-846A-1
Sequence 2, Application US/10084846A Publication No. US20040006026A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/10084846A Publication No. US20040006026A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/084,846A CURRENT FILING DATE: 2003-02-25 PRIOR APPLICATION NUMBER: PCT/EP01/09815 PRIOR FILING DATE: 2001-08-24 PRIOR APPLICATION NUMBER: DE 101 09 166.4 PRIOR FILING DATE: 2001-02-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 120
SOFTWARE: PatentIn Ver. 3
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BECHTHOLD, ANDREAS
TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
FILE REFERENCE: 1974-005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: WEITNAUER, GABRIELE APPLICANT: MUHLENWEG, AGNES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Streptomyces viridochromogenes
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Similarity 49.6%;
32; Conservative
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Pred. No. 0.0013;
0; Mismatches 134;
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APPLICANT: TREFZER, AXEL
APPLICANT: BECHTHOLD, ANDREAS
ITILE OF INVENTION: AVILAMYCIN DERIVATIVES
FILE REFERENCE: 1974-005
CURRENT APPLICATION NUMBER: US/10/084,846A
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: DETT/EPO1/09815
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: DE 101 09 166.4
PRIOR FILING DATE: 2001-02-25
NUMBER OF SEQ ID NOS: 120
SOFTWARE: PALENTIN Ver. 3.2
SEQ ID NO 2
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; TYPE: DNA
; ORGANISM: Streptomyces viridochromogenes
US-10-084-846A-2
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Best Local Similarity
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TGGCCGCGGTGCTGCGCGCGCACCCC 13952
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Pred. No. 0.0013;
0; Mismatches 134;
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GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262 SEQ ID NO 6879 LENGTH: 1185 Sequence 6879, Application US/10156761 Publication No. US20030119018A1 LOCATION: (1). -10-156-761-6879 CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109 ORGANISM: Streptomyces FEATURE: NAME/KEY: CDS TYPE: DNA

Query M Best Lo Matches	Match 4.0%; Score 51; DB 14; Length 1185; Local Similarity 45.0%; Pred. No. 0.00029; es 230; Conservative 0; Mismatches 280; Indels 1; Gaps 1;
Ş	182 ACAGCCACCAGCGGGCACAGCTCATGGCCCTGCTGTCGCGGGATGGGTCCCCGGTCGGT
g	503 ACCGCCGCCTGCGCCCCCCCAGGAGCGGCTCCCGGCCCGGGTGACCGTCGAGAACG 562
Ϋ́	242 GCAGCCGTGACGCTGCGGTGCAGGTGAACCCGCGCGCGCG
В	563 AGACCAACCTCGCCGCCCTGGCCGAACAGCGCGAGGGCGCGCGC
Ωy	302 TCGGGCGCGCACGCTGCAGCCTGCAGGGTGCCGAGCCCGAGCCCCGATCGGGTT 361
망	623 TOGTGCTGCTGTGGCCACGGCACCGGCACCGGCGGCCGTCCTCGACGGCAGACTCC 682
Qγ	362 CCTGTCAACCCCGTGGCCACGCGGCGCGCGGGAGATCCCGCGATCCTGGCAGACCGTAG 421
дb	683 GCCGTGGCCCTCGGGCGCACCGGCGAATCGGCTTCCTGCCGGTACCGGGTACCGGCC 742
γŞ	422 CCCCGTTCTCGTCGTCACCTTCTGTGGCCTCTCCTCCTCACTGGAGGTTGCGGGAGGCA 481
дb	743 CACTGCCCTCGGCGACGGACTGCGAGGGCGGCTTCCACTGACTG
Ωy	482 GGCAGACACCCACGAAGGGAGAGGGGAGCCCGGGATCCTCGGGGACCCGGGAACCGGAGC 541
дb	803 TCGCCCGGCTGGCGAGGGAGCACGGCTCGTGGCGGCCGGGCCGATGAGCCGCAGG 862
γQ	542 CGAGAGAGGTGG-CCGCGAGGAAAGCGGTCCCCCAGCCGCGAAGCGAA
qq	863 CGGCGGCGCTGCTGCGGGCGGCGGCGGCGCGCGCGCGCG
γ	601 CAGGCTGCAGGGCAGGCGGGTGGGAGCAGCAGCAGCCGGGAGGACCAGGAGCAGTGTG 660
В	923 TCGACGTCCTCGCCGACCGCCATCGCCATCGCCGCCGCCGTCGTGGCCGTCCTGGACC 982
γ	661 GCGGCGATGCAGTCTGAGCCTGGGAGCGAGC 691
g	983 CCGGCTGTGTGGTCCTGGCCGAGGTCGG 1013
Search co Job time	completed: April 6, 2004, 20:47:15 e : 538 secs

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Aaa71703 Human cal	AAA71703	62	. 8 7	49
Aav42685 DNA encod	AAV42685	62	. 8 7	49
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Aav29059 Human cal	AAV29059	99	.8 7	49

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05-SE AAD00 AAD00:

Mouse oocyte-specific O1-180 cDNA clone

Oocyte-specific; ovary; O1-180; mouse; gynaecological; treatment; screen; cell proliferative disorder; cell degenerative disorder; contraceptive; modulator; signalling pathway; human infertility; cancer; ovulation; ss. ďB

04-MAY-2000 WO200024755-A1. Location/Qualifiers 28. .1113 /product= "Mouse oocyte-specific protein,

01-180"

28-OCT-1998; (BAYU) BAYLOR COLLEGE MEDICINE 98US-0106020P

28-OCT-1999;

99WO-US025209

Matzuk MM, Wang ٦,

WPI; 200 P-PSDB;

2000-350684/30. DB; AAY70948.

O1-180, O1-184 and O1-236 polypeptides and nucleic acids encoding useful for evaluating potential contraceptives to block ovulation reversible manner. them,

Claim 2; Fig 1; 54pp; English.

The present sequence is the cDNA encoding the mouse cocyte-specific protein O1-180, expressed in the cocytes of primary (one-layer) preantral follicles through ovulation. It provides in vitro and in vivo reagents for studying ovarian development and function. This sequence has

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gynaecological and contraceptive activity. Agents which modulate O1-180, O1-184 and O1-236 may be used to treat cell proliferative or degenerative disorders, associated with abnormal expression of these ovary specific genes. This ovary-specific sequence can be used as reagents to evaluate potential contraceptives, to block ovulation in a reversible manner. It is also used to screen for genetic mutations in signalling pathways, that are associated with some forms of human infertility or gynaecological
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New ovary-specific-genes decreasing conception or composition for treating
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The present sequence is that of murine ovary-specific O1-180 cDNA CC obtained from a mouse ovary cDNA library. O1-180 clones were initially condensified in a subtractive hybridisation screen using ovaries from Gdf9 cc identified in a subtractive hybridisation screen using ovaries from Gdf9 cc knockout and wild-type mice. The O1-180 gene (see ABZ24590) on chromosome CC is also provided. Loss of O1-180 results in female infertility and cc subfertility. The invention provides ovary-specific and cocyte-specific cc murine and human O1-180, O1-184 and O1-236 polymicleotides and cocyte-specific cc polypeptides. These genes and their protein products appear to relate to compours cell proliferative or degenerative disorders, especially those cc involving ovarian tumours, such as gremative disorders, and granulosa cell ct tumours, or infertility, such as premature ovarian fallure. The invention crowides a method for detection of as cell proliferative or degenerative of sorder of the ovary, which is associated with the expression of O1-180, O1-184 or O1-236. It also provides a method for treating such disorders cof o1-180, O1-184 or O1-236, and a method of screening for compounds that compounds are possible contraceptive or fertility enhancing agents. These compounds are possible contraceptive or fertility enhancing capents. The modulator is preferably a polypeptide, small molecule or compounded as the contraceptive or fertility enhancing agents.
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                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                           ACCCGCGCCCCCCTCCTTCCCCCGGCTACAGACAGCTCATGGCCGCGGAGTACGTCGA
                                                                                                       TCCTTATCCGCAGGCCAACCAAAGCCGGGGATGGCTGCAGGTTCGGAGCCAGGGGCTGCCG
                                                                                                                                     TCCTTATCCGCAGGCCACCAAAGCCGGGGATGGCTGGAGGTTCGGAGCCAGGGGCTGCCG
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                                                                                                                                                                                                                                                                                                                                 of novel murine ovary-specific gene 01-180 (see ABZ24590). The major of inference between the 01-180 gene and pseudogene is a 13-nucleotide gap in exon 1 of the pseudogene, which is expected to cause a frameshift and carly termination in exon 2 of the pseudogene. The sequences of exon 2 are identical in the 01-180 gene and pseudogene. The sequences of exon 2 mutations in exons 3 and 4. The invention provides ovary-specific and cocyte-specific murine and human 01-180, 01-184 and 01-236 polynucleotides and polypeptides. These genes and their protein products polynucleotides and polypeptides. These genes and their protein products appear to relate to various cell proliferative or degenerative disorders, especially those involving ovarian tumours, such as germ line tumours and granulosa cell tumours, or infertility, such as premature ovarian can modulator compounds are provided. Modulators also have contraceptive or fertility enhancing activities
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CAGCCGTGACGCTGCGGTGCAGGTGAACCCGCGCGCGCGACGCCTCGGTGCAGTGTTCACT
                                                           TCCTTATCCGCAGGCCACCAAAGCCGGGGATGGCTGGAGGTTCGGAGCCAGGGGCTGCCG
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Pred. No. 4.8e-169;
0; Mismatches 7;
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New ovary-specific-genes comprising O1-180 or decreasing conception or enhancing fertility, composition for treating e.g. cancer.

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Matches 207
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The specification describes antisense oligonucleotides (AAX52869-X55271)

The specification describes antisense oligonucleotides (AAX52869-X55271)
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                                                                                                                                                                                 The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, tugal or viral infection. The present sequence was used to
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Katagiri
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                                                      The specification describes antisense oligonucleotides (AAX52869-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and concoding regions of RNAs corresponding to target genes, coding and codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
CC end and the juxta-section between coding and non-coding regions and all conditions or mixtures. The antisense oligonucleotides may be derived conditions or mixtures. The antisense oligonucleotides may be derived compared to the sequences AAX55272-74. These multiple target oligonucleotides (specifically AAX5180-271) can be used for the antisense treatment of cliseases and conditions. Typical diseases and conditions are those cassociated with impaired respiration and inflammation, including lung cliseases, pulmonary vasoconstriction, inflammation, allergic rhinitis, cut associated with impaired respiration, inflammation, allergic rhinitis, coliseases (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g. colon cancer, bain, cystic fibrosis, pulmonary hypertension, coliseases (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic cancer, entanoma, hepatic metastasses, as well as all types of cancers which may metastasize or have metastasized to the lungs, including breast and prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                impaired respiration; inflammation; lung disease; pulmonary vasoconstriction; inflammation; altergic rhinitis; pulmonary vasoconstriction; inflammation; altergic rhinitis; acute asthma, altergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary hypertension; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer;
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Best Local S
Matches 132
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                                                                                                                                                                                                                                                                                                                                    Sequence 987 BP; 121 A; 358 C; 371 G; 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New avilamycin derivatives, useful for treatment of infections, and nucleic acid encoding avilamycin synthesis enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 13; Page 244-248; 319pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Weitnauer G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-FEB-2001; 2001DE-01009166
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                                                                               AGCTCATGGCCCTGCTGTCGCGGATGGGTCCCCGGTCAGCAGCCGTGACGCTGCGG
                                                                                                                                                                   TCGACCACGTCTTCGGCGGACTTCTTCGCGTACCTGGCGGACGACCCGACCTGTCGT
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 TGGCCGCGGTGCTGCGCGCGCACCCC
                            AGCCTGCAGGGTGCCGAGCCAGCCCC 345
                                                      ACCAGGACTTCTCCGGCGCCCCCCCGCGGTGGACGTCGGGGGGCGGGGACGGGACGCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BIOPHARM
                                                                                                                                                                                                                                                                                           4.0%;
                                                                                                                                                                                                                                                                              Score 51.6; DB 7;
Pred. No. 0.029;
0; Mismatches 134;
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DNA;

59816

98

(first entry)

Streptomyces viridochromogenes Avi gene cluster sense strand

RESULT 11
ABZ37516 standard; D
XX
AC ABZ37516;

DT 26-FEB-2003 (first
XX
DT 26-FEB-2003 viridoc
XX
Expression; antibact
KW Avilamycin; antibact
KW medicine; Staphyloco
XX
PM Streptomyces viridoc
XX
PM W0200268436-A1.
XX
PD 06-SEP-2002. Avilamycin; antibacterial; virucide; protozoacide; fungicide; medicine; Staphylococcus aureus; biosynthetic gene cluster; g

Streptomyces viridochromogenes

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RESULT 12
ABZ37515
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to avilamycin derivatives (I) with antibacterial, virucide, protozoacide and fungicide activity. (I) are useful for treatment of infections (bacterial, viral, protozoal or fungal), in human or veterinary medicine, particularly where caused by Staphylococcus aureus. (I) are more hydrophilic than known avilamycins. The present sequence is that of a nucleic acid encoding avilamycin synthesis enzymes from the Streptomyces viridochromogenes Avilamycin A biosynthetic gene cluster (ABZ37515-ABZ37516)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 59816 BP; 8760 A; 21053 C; 21088 G; 8915 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New avilamycin derivatives, useful for treatment of nucleic acid encoding avilamycin synthesis enzymes.
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24-AUG-2001; 2001WO-EP009815
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                                                     06-SEP-2002.
                                                                                                  WO200268436-A1
                                                                                                                                                                                                                                                                       Streptomyces viridochromogenes Avi gene cluster sense strand.
                                                                                                                                                                                                                                                                                                                             05-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                          ABZ37515
                                                                                                                                                     Streptomyces viridochromogenes
                                                                                                                                                                                                                          Avilamycin; antibacterial; virucide;
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                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                          DNA;
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                                                                                                                                                                                                  aureus; biosynthetic
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                                                                                                                                                                                                                          protozoacide;
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                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 59816;
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09-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                               AAV44436;
     11-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV44436
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Query Match
Best Local Similarity
Matches 132; Conserv
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                                        07-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 59816 BP; 8915 A; 21088 C; 21053 G; 8760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New avilamycin derivatives, useful for treatment of nucleic acid encoding avilamycin synthesis enzymes.
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                                                                                                                                                                     Mycobacterium
                                                                                                                                                                                                           Tuberculosis;
                                                                                                                                                                                                                                                      Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                       standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCTCTACAACGCGGCGATGAGCCAGGGCACCGGTGGGATCGCCGGCCTGGTCGCGGCGC
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(first entry)
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                                                                                                                                                                     tuberculosis; strain
                                                                                                                                                                                                             infection; diagnosis;
                                                                                                                                                                                                                                                      tuberculosis antigen
                                        97WO-US018214.
96US-00729622
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Pred. No. 0.11;
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RESULT 14
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AC AAV64
AC AAV64
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis antigen XF22; 3' DNA is provided in AAV44437. XF22 DNA was isolated from a M. tuberculosis strain Erdman genomic DNA expression library using sera from patients having extrapulmonary tuberculosis. It bears no similarity to known sequences. The invention relates to methods and compositions for diagnosing tuberculosis. It provides polypeptides (see AAW64291-W6479) comprising an antigenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of a M. tuberculosis antigen, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using these polypeptides, antibodies or oligonuclectide probes and primers. (Updated on 17-OCT-2003 to standardise OS field)
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Vedvick TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 400 BP; 74 A; 151 C; 162 G; 13 T; 0
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                                                            Mycobacterium
                                                                                                               Tuberculosis; immunogenic; soluble;
vaccine; pharmaceutical; infection;
                                                                                                                                                                                                                                                                                                                   AAV64545
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                                                                                                                                                                                                   tuberculosis immunogenic polypeptide XP22 5'-end
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S, Twardzik
                                                                                                                                                                                                                                                            (first entry)
                                                               tuberculosis
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Pred. No. 0.064;
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0; Mismatches
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                                                                                                                  antigen; protective diagnosis; ss.
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RESULT 11
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Matches 130;
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                                                                                                                                          Antigen; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence encodes an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reed SG,
Vedvick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunogenic Mycobacterium tuberculosis polypeptide(s) develop products for the detection of M. tuberculosis diagnosis, treatment and prevention of tuberculosis.
                                                                                                                                                                                                            M. tuberculosis recombinant antigen DNA encoding
                                                                                                                                                                                                                                                               05-NOV-1999
                                                                                                                                                                                                                                                                                                                                                         AAZ19134 standard; DNA; 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 400 BP; 74 A; 151 C; 162 G; 13 T; 0 U; 0 Other;
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13-MAR-1997;
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S, Twardzik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                               (first entry)
                                                                                               tuberculosis.
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97US-00818112
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                                                                                                                                                                    detection;
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                                                                                                                                                                    infection; antibody;
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                                                                                                                                                                         immunisation;
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infection
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Best Local Similarity 49.2%;
Matches 130; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reed SG, Skeiky YAW, Dillon DC, Covedvick TS, Twardzik DR, Lodes MJ,
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05-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 400 BP; 74 A; 151 C; 162 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 215-216; 323pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptide comprising antigenic portions of M. tuberculosis
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                                                                                                                        CTTCACCCAAGGCGCCGACGGCAACGCCGGCAACGGCGGTGACGGCGGGGTCGGCGGCAA 178
                                                            CGGCGGCGACGGTGCACTCTCAGG
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98US-00072596.
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J, Hendrickson RC;
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